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(54) Title: NUCLEIC ACID MOLECULES ENCODING PLANT CELL CYCLE PROTEINS AND USES THEREFOR

(57) Abstract: The invention provides isolated nucleic acids molecules, designated CCP nucleic acid molecules, which encode novel cell cycle associated polypeptides. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing CCP nucleic acid molecules, host cells into which the expression vectors have been introduced, and transgenic plants in which a CCP gene has been introduced or disrupted. The invention still further provides isolated CCP proteins, fusion proteins, antigenic peptides and anti-CCP antibodies. Agricultural, diagnostic, screening, and therapeutic methods utilizing compositions of the invention are also provided.

WO 01/85946 A2

NUCLEIC ACID MOLECULES ENCODING PLANT CELL CYCLE PROTEINS AND USES THEREFOR

Related Applications

This application claims priority to U.S. provisional patent application serial number 60/204,045, filed May 12, 2000. The contents of this provisional patent application are incorporated herein by reference in their entirety.

Background of the Invention

Cell division plays a crucial role during all phases of plant development. The continuation of organogenesis and growth responses to a changing environment require precise spatial, temporal, and developmental regulation of cell division.

The basic mechanisms controlling the progression through the cell cycle appear to be conserved in all higher eukaryotes, although the temporal and spatial control of cell division can differ largely between organisms. Plants have unique developmental features which are not found in either animals or fungi. First, due to the presence of a rigid cell wall, plant cells cannot move and consequently organogenesis is dependent on cell division and cell expansion at the site of formation of new organs. Secondly, cell divisions are confined to specialized regions, called meristems. These meristems continuously produce new cells which, as they move away from the meristem, become differentiated. The meristem identity itself can change from a vegetative to a reproductive phase, resulting in the formation of flowers. Thirdly, plant development is largely post-embryonic. During embryogenesis, the main developmental event is the establishment of the root-shoot axis. Most plant growth occurs after germination, by iterative development at the meristems. Lastly, as a consequence of the sessile life of plants, development and cell division are, to a large extent, influenced by environmental factors such as light, gravity, wounding, nutrients, and stress conditions. All these features are reflected in a plant-specific regulation of the factors controlling cell division.

The unparalleled potential of plants for continuous organogenesis and plastic growth also relies on the competent or active state of the cell division apparatus. The discovery of a common mechanism underlying the regulation of the cell cycle in yeasts and animals has led to efforts to extend these findings to the plant kingdom and is leading to research aimed at converting the gathered knowledge into useful traits introduced in transgenic plants.

When eukaryotic cells and, thus, also plant cells divide they go through a highly ordered sequence of events collectively termed as the "cell cycle." Briefly, DNA replication or synthesis (S) and mitotic segregation of the chromosomes (M) occur with intervening gap phases (G1 and G2) and the phases follow the sequence G1-S-G2-M. Cell

division is completed after cytokinesis, the last step of the M-phase. Cells that have exited the cell cycle and have become quiescent are said to be in the G0 phase. Cells at the G0 stage can be stimulated to reenter the cell cycle at the G1 phase. The transition between the different phases of the cell cycle are basically driven by the sequential
5 activation/inactivation of a kinase (called "cyclin-dependent kinase", "CDC" or "CDK") by different agonists.

Proteins called cyclins are required for kinase activation. Cyclins are also important for targeting the kinase activity to a given subset of substrate(s). Other factors regulating CDK activity include CDK inhibitors (CKIs or ICKs, KIPs, CIPs, INKs), CDK
10 activating kinase (CAK) and CDK phosphatase (CDC25) (Mironov *et al.* (1999) *Plant Cell* 11, 509-522 and Won K. *et al.* (1996) *EMBO J.* 15, 4182-4193).

Summary of the Invention

The present invention is based, at least in part, on the discovery of novel plant
15 nucleic acid molecules and polypeptides encoded by such nucleic acid molecules, referred to herein as "cell cycle proteins" or "CCP." The CCP nucleic acid and polypeptide molecules of the present invention are useful as modulating agents in regulating cell cycle progression in, for example, plants. Accordingly, in one aspect, this invention provides isolated nucleic acid molecules encoding CCP polypeptides, as well as nucleic acid
20 fragments suitable as primers or hybridization probes for the detection of CCP-encoding nucleic acids.

In one embodiment, a CCP nucleic acid molecule of the invention is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more identical to the nucleotide sequence (e.g., to the entire length of the nucleotide sequence) of SEQ ID NO:1-66 or 228-239, or a
25 complement thereof.

In a preferred embodiment, the isolated nucleic acid molecule includes the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239, or a complement thereof. In another preferred embodiment, an isolated nucleic acid molecule of the invention encodes the amino acid sequence of a plant CCP polypeptide.

30 Another embodiment of the invention features nucleic acid molecules, preferably CCP nucleic acid molecules, which specifically detect CCP nucleic acid molecules relative to nucleic acid molecules encoding non-CCP polypeptides. For example, in one embodiment, such a nucleic acid molecule is at least 15, 20, 25, 30, 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, or 800 nucleotides in length and
35 hybridizes under stringent conditions to a nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239, or a complement thereof.

In other preferred embodiments, the nucleic acid molecule encodes a naturally occurring allelic variant of a plant CCP polypeptide, wherein the nucleic acid molecule

hybridizes to the nucleic acid molecule of SEQ ID NO:1-66 or 228-239 under stringent conditions.

Another embodiment of the invention provides an isolated nucleic acid molecule which is antisense to a CCP nucleic acid molecule, *e.g.*, the coding strand of a CCP nucleic acid molecule.

Another aspect of the invention provides a vector comprising a CCP nucleic acid molecule. In certain embodiments, the vector is a recombinant expression vector. In another embodiment, the invention provides a host cell containing a vector of the invention. The invention also provides a method for producing a CCP polypeptide, by culturing in a suitable medium a host cell of the invention, *e.g.*, a plant host cell such as a host monocot plant cell (*e.g.*, rice, wheat or corn) or a dicot host cell (*e.g.*, *Arabidopsis thaliana*, oilseed rape, or soybeans) containing a recombinant expression vector, such that the polypeptide is produced.

Another aspect of this invention features isolated or recombinant CCP polypeptides. In one embodiment, an isolated CCP polypeptide has one or more of the following domains: a "cyclin destruction box", a "cyclin box motif 1", a "cyclin box motif 2", a "CDC2 motif", a "CDK phosphorylation site", a "nuclear localization signal", a "Cy-like box", an "Rb binding domain", a "DEF domain", a "DNA binding domain", a "DCB1 domain", a "DCB2 domain" and/or a "SAP domain".

In a preferred embodiment, a CCP polypeptide includes at least one or more of the following domains: a "cyclin destruction box", a "cyclin box motif 1", a "cyclin box motif 2", a "CDC2 motif", a "CDK phosphorylation site", a "nuclear localization signal", a "Cy-like box", an "Rb binding domain", a "DEF domain", a "DNA binding domain", a "DCB1 domain", a "DCB2 domain" and/or a "SAP domain", and has an amino acid sequence at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or more identical to the amino acid sequence of SEQ ID NO:67-132, 205, 211, 215-216, or 220-227.

In another preferred embodiment, a CCP polypeptide includes at least one or more of the following domains: a "cyclin destruction box", a "cyclin box motif 1", a "cyclin box motif 2", a "CDC2 motif", a "CDK phosphorylation site", a "nuclear localization signal", a "Cy-like box", an "Rb binding domain", a "DEF domain", a "DNA binding domain", a "DCB1 domain", a "DCB2 domain" and/or a SAP domain and has a CCP activity (as described herein).

In yet another preferred embodiment, a CCP polypeptide includes one or more of the following domains: a "cyclin destruction box", a "cyclin box motif 1", a "cyclin box motif 2", a "CDC2 motif", a "CDK phosphorylation site", a "nuclear localization signal", a "Cy-like box", an "Rb binding domain", a "DEF domain", a "DNA binding domain", a "DCB1 domain", a "DCB2 domain" and/or a SAP domain and is encoded by a nucleic acid

molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-66 or 228-239.

5 In another embodiment, the invention features fragments of the polypeptide having the amino acid sequence of SEQ ID NO:67-132, 205, 211, 215-216, or 220-227, wherein the fragment comprises at least 15 amino acids (*e.g.*, contiguous amino acids) of the amino acid sequence of SEQ ID NO:67-132, 205, 211, 215-216, or 220-227. In another embodiment, a CCP polypeptide has the amino acid sequence of SEQ ID NO:67-132, 205, 211, 215-216, or 220-227.

10 In another embodiment, the invention features a CCP protein which is encoded by a nucleic acid molecule consisting of a nucleotide sequence at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or more identical to a nucleotide sequence of SEQ ID NO:1-66 or 228-239, or a complement thereof. This invention further features a CCP polypeptide, which is encoded by a nucleic acid molecule consisting of a
15 nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-66 or 228-239, or a complement thereof.

In another embodiment the invention provides transgenic plants (*e.g.*, monocot or dicot plants) containing an isolated nucleic acid molecule of the present invention. For
20 example, the invention provides transgenic plants containing a recombinant expression cassette including a plant promoter operably linked to an isolated nucleic acid molecule of the present invention. The present invention also provides transgenic seed from the transgenic plants. In another embodiment the invention provides methods of modulating, in a transgenic plant, the expression of the nucleic acids of the invention.

25 The proteins of the present invention or portions thereof, *e.g.*, biologically active portions thereof, can be operatively linked to a non-CCP polypeptide (*e.g.*, heterologous amino acid sequences) to form fusion proteins. The invention further features antibodies, such as monoclonal or polyclonal antibodies, that specifically bind polypeptide of the invention, preferably CCP polypeptide. In addition, the CCP polypeptide or biologically
30 active portions thereof can be incorporated into pharmaceutical compositions, which optionally include pharmaceutically acceptable carriers.

In another aspect, the present invention provides a method for detecting the presence of a CCP nucleic acid molecule, polypeptide in a biological sample by contacting the biological sample with an agent capable of detecting a CCP nucleic acid molecule,
35 polypeptide such that the presence of a CCP nucleic acid molecule, polypeptide is detected in the biological sample.

In another aspect, the present invention provides a method for detecting the presence of CCP activity in a biological sample by contacting the biological sample with

an agent capable of detecting an indicator of CCP activity such that the presence of CCP activity is detected in the biological sample.

In another aspect, the invention provides a method for modulating CCP activity comprising contacting a cell capable of expressing CCP with an agent that modulates CCP activity such that CCP activity in the cell is modulated. In one embodiment, the agent inhibits CCP activity. In another embodiment, the agent stimulates CCP activity. In one embodiment, the agent is an antibody that specifically binds to a CCP polypeptide. In another embodiment, the agent modulates expression of CCP by modulating transcription of a CCP gene or translation of a CCP mRNA. In yet another embodiment, the agent is a nucleic acid molecule having a nucleotide sequence that is antisense to the coding strand of a CCP mRNA or a CCP gene.

In one embodiment, the methods of the present invention are used to increase crop yield, improve the growth characteristics of a plant (such as growth rate or size of specific tissues or organs in the plant), modify the architecture or morphology of a plant, improve tolerance to environmental stress conditions (such as drought, salt, temperature, nutrient or deprivation), or improve tolerance to plant pathogens (*e.g.*, pathogens that abuse the cell cycle) by modulating CCP activity in a cell. In one embodiment, the CCP activity is modulated by modulating the expression of a CCP nucleic acid molecule. In yet another embodiment, the CCP activity is modulated by modulating the activity of a CCP polypeptide. Modulators of CCP activity include, for example, a CCP nucleic acid or polypeptide.

The present invention also provides diagnostic assays for identifying the presence or absence of a genetic alteration characterized by at least one of (i) aberrant modification or mutation of a gene encoding a CCP polypeptide; (ii) mis-regulation of the gene; and (iii) aberrant post-translational modification of a CCP polypeptide, wherein a wild-type form of the gene encodes a protein with a CCP activity.

In another aspect the invention provides methods for identifying a compound that binds to or modulates the activity of a CCP polypeptide, by providing an indicator composition comprising a CCP polypeptide having CCP activity, contacting the indicator composition with a test compound, and determining the effect of the test compound on CCP activity in the indicator composition to identify a compound that modulates the activity of a CCP polypeptide. The identified compounds may be used as herbicides or plant growth regulators.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Brief Description of the Drawings

Figure 1 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP1. The complete nucleotide sequence (Figure 1A) corresponds to nucleic acids 1 to 1715 of SEQ ID NO:39. The complete amino acid sequence (Figure 1B) corresponds to amino acids 1 to 460 of SEQ ID NO:105. Underlined in Figure 1A and Figure 1B are the partially characterized nucleotide (SEQ ID NO:1) and predicted partial amino acid (SEQ ID NO:67) sequence, respectively. Further indicated in Figure 1A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP1 by PCR. The SEQ ID NOs of the primers used can be found in Table III. Indicated in Figure 1B are the cyclin destruction box (black shaded box) and the cyclin box motifs 1 and 2 (both in gray shaded boxes).

Figure 2 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP2. The complete nucleotide sequence corresponds to nucleic acids 1 to 2195 of SEQ ID NO:40. Underlined is the partially characterized nucleotide (SEQ ID NO:2) sequence. Nucleotide sequence differences between SEQ ID NO:40 and SEQ ID NO:2 are depicted. Indicated are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP2 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 3 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP2. The complete amino acid sequence corresponds to amino acids 1 to 664 of SEQ ID NO:106. Underlined is the predicted partial amino acid (SEQ ID NO:68) sequence.

Figure 4 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP3. The complete nucleotide sequence (Figure 3A) corresponds to nucleic acids 1 to 1413 of SEQ ID NO:41. The complete amino acid sequence (Figure 3B) corresponds to amino acids 1 to 450 of SEQ ID NO:69. Underlined in Figure 3A and Figure 3B are the partially characterized nucleotide (SEQ ID NO:3) and predicted partial amino acid (SEQ ID NO:69) sequences, respectively. Indicated in Figure 3A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP3 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:41

and SEQ ID NO:3 are depicted. Indicated in Figure 3B are the cyclin destruction box (black shaded box) and the cyclin box motifs 1 and 2 (both in gray shaded boxes).

Figure 5 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP4. The complete nucleotide sequence (Figure 5A) corresponds to nucleic acids 1 to 672 of SEQ ID NO:4. The complete amino acid sequence (Figure 5B) corresponds to amino acids 1 to 223 of SEQ ID NO:70. Indicated in Figure 5A are stop and start codon (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP4 by PCR. SEQ ID NOs of the primers used can be found in Table III. Indicated in Figure 5B is the CDK phosphorylation site (black shaded box).

Figure 6 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP5. The complete nucleotide sequence (Figure 6A) corresponds to nucleic acids 1 to 1287 of SEQ ID NO:5. The complete amino acid sequence (Figure 6B) corresponds to amino acids 1 to 429 of SEQ ID NO:71. Indicated in Figure 6A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP5 by PCR. SEQ ID NOs of the primers used can be found in Table III. Indicated in Figure 6B are the cyclin destruction box (black shaded box) and the cyclin box motifs 1 and 2 (both in gray shaded boxes).

Figure 7 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP6. The complete nucleotide sequence corresponds to nucleic acids 1 to 2766 of SEQ ID NO:42. Underlined is the partially characterized nucleotide (SEQ ID NO:6) sequence. Indicated are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP6 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:42 and SEQ ID NO:6 are depicted.

Figure 8 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP6. The complete amino acid sequence corresponds to amino acids 1 to 901 of SEQ ID NO:108. Underlined is the predicted partial amino acid (SEQ ID NO:72) sequence.

Figure 9 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP7/CCP8. The complete nucleotide sequence (Figure 9A) corresponds to nucleic acids 1 to 1260 of SEQ ID NO:43. The complete amino acid sequence (Figure 9B) corresponds to amino acids 1 to 358 of SEQ ID NO:109. Underlined

in Figure 9A and Figure 9B are the partially characterized nucleotide (SEQ ID NO:7) and predicted partial amino acid (SEQ ID NO:73) sequence, respectively. Italic sequences in Figure 9A and Figure 9B correspond to the partially characterized nucleotide (SEQ ID NO:8) and amino acid (SEQ ID NO:74) sequence, respectively, of another clone found independently to interact with an AtE2F protein in a yeast two-hybrid screen. Indicated in Figure 9A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP7/8 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:43 and SEQ ID NO:7-8 are depicted.

Figure 10 depicts the cDNA sequence and predicted amino acid sequence of the Arabidopsis thaliana CCP9. The complete nucleotide sequence (Figure 10A) corresponds to nucleic acids 1 to 1308 of SEQ ID NO:9. The complete amino acid sequence (Figure 10B) corresponds to amino acids 1 to 436 of SEQ ID NO:75. Indicated in Figure 10A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP9 by PCR. SEQ ID NOs of the primers used can be found in Table III. Indicated in Figure 10B are the cyclin destruction box (black shaded box) and the cyclin box motifs 1 and 2 (both in gray shaded boxes).

Figure 11 depicts the cDNA sequence and predicted amino acid sequence of the Arabidopsis thaliana CCP10. The complete nucleotide sequence (Figure 11A) corresponds to nucleic acids 1 to 1006 of SEQ ID NO:10. The complete amino acid sequence (Figure 11B) corresponds to amino acids 1 to 254 of SEQ ID NO:76. Indicated in Figure 11A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP10 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 12 depicts the cDNA sequence and predicted amino acid sequence of the Arabidopsis thaliana CCP11. The complete nucleotide sequence (Figure 12A) corresponds to nucleic acids 1 to 653 of SEQ ID NO:44. Indicated in Figure 12A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP11 by PCR. SEQ ID NOs of the primers used can be found in Table III. However, during prediction of the open reading frame a frame shift was introduced which effected the CCP11 open reading frame. The stop codon indicated in italics in a black shaded box is the putative correct stop codon.

The amino acid sequence in Figure 12B corresponds to amino acids 1 to 86 of SEQ ID NO:77, the protein encoded by the initially identified open reading frame of SEQ ID NO:11. The putative correct complete amino acid sequence in Figure 12C corresponds to amino acids 1 to 98 of SEQ ID NO:110.

5 *Figure 13* depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP12/13. The complete nucleotide sequence (Figure 13A) corresponds to nucleic acids 1 to 1266 of SEQ ID NO:45. The complete amino acid sequence (Figure 13B) corresponds to amino acids 1 to 385 of SEQ ID NO:111. Double underlined in Figure 13A and Figure 13B are the partially characterized 3' nucleotide
10 (SEQ ID NO:12) and C-terminal predicted partial amino acid (SEQ ID NO:78) sequence, respectively. Single underlined in Figure 13A and Figure 13B are the partially characterized 5' nucleotide (SEQ ID NO:13) and N-terminal predicted partial amino acid (SEQ ID NO:79) sequences, respectively. Indicated in Figure 13A are the stop and start codons (both in black shaded boxes) and the primers (grey shaded boxes) used to amplify
15 the coding region of CCP12/13 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:45 and SEQ ID NO:12 are depicted.

Figure 14 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP14. The complete nucleotide sequence (Figure 14A)
20 corresponds to nucleic acids 1 to 1520 of SEQ ID NO:46. The complete amino acid sequence (Figure 14B) corresponds to amino acids 1 to 465 of SEQ ID NO:112. Underlined in Figure 14A and Figure 14B are the partially characterized nucleotide (SEQ ID NO:14) and predicted partial amino acid (SEQ ID NO:80) sequence, respectively. Indicated in Figure 14A are the stop and start codons (both in black shaded boxes) which
25 are part of the primers (grey shaded boxes) used to amplify the coding region of CCP14 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 15 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP15. The complete nucleotide sequence (Figure 15A)
30 corresponds to nucleic acids 1 to 1142 of SEQ ID NO:47. The complete amino acid sequence (Figure 15B) corresponds to amino acids 1 to 313 of SEQ ID NO:113. Underlined in Figure 15A and Figure 15B are the partially characterized nucleotide (SEQ ID NO:15) and predicted partial amino acid (SEQ ID NO:81) sequence, respectively. Indicated in

Figure 15A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP15 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:47 and SEQ ID NO:15 are depicted. Indicated in Figure 15B are the PSTTLRE motif (boxed) characteristic for the subclass of plant PSTTLRE CDC2 kinases. Further indicated in Figure 15B are three CDC2 motifs (black shaded box, grey shaded box and double underlined). Other residues conserved in CDC2s are underscored by '*' (residues in common with ProDom domain PD198850), '+' (residues in common with ProDom domain PD015684), '-' (residues in common with ProDom domain PD063669), and '1' (residues in common with ProDom domain PD195780).

Figure 16 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP16. The complete nucleotide sequence (Figure 16A) corresponds to nucleic acids 1 to 1189 of SEQ ID NO:48. The complete amino acid sequence (Figure 16B) corresponds to amino acids 1 to 292 of SEQ ID NO:114. Indicated in Figure 16A are the stop and the three possible start codons (all in black shaded boxes) and the primers (grey shaded boxes) used to amplify the coding region of CCP16 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:48 and SEQ ID NO:16 are depicted. Indicated in Figure 16B are the DNA binding domain (black shaded box), DEF domain (grey shaded box), DCB1 domain (single underlined) and DCB2 domain (double underlined), all domains characteristic for a DP protein.

Figure 17 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP17. The complete nucleotide sequence (Figure 17A) corresponds to nucleic acids 1 to 794 of SEQ ID NO:17. The complete amino acid sequence (Figure 17B) corresponds to amino acids 1 to 173 of SEQ ID NO:83. Indicated in Figure 17A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP17 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 18 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP18. The complete nucleotide sequence (Figure 18A) corresponds to nucleic acids 1 to 805 of SEQ ID NO:49. The complete amino acid sequence (Figure 18B) corresponds to amino acids 1 to 165 of SEQ ID NO:115.

Underlined in Figure 15A and Figure 15B are the partially characterized nucleotide (SEQ ID NO:18) and predicted partial amino acid (SEQ ID NO:84) sequence, respectively. Indicated in Figure 18A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP18 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 19 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP19. The complete nucleotide sequence (Figure 19A) corresponds to nucleic acids 1 to 1152 of SEQ ID NO:19. The complete amino acid sequence (Figure 1B) corresponds to amino acids 1 to 383 of SEQ ID NO:85. Indicated in Figure 19A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP19 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 20 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP20/21. The complete nucleotide sequence corresponds to nucleic acids 1 to 1539 of SEQ ID NO:50. Underlined are the partially characterized 5' nucleotide (SEQ ID NO:20) sequence and the partially characterized 3' nucleotide (SEQ ID NO:21). Indicated in Figure 20 are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP20/21 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NOs:20-21 and SEQ ID NO:50 are depicted.

Figure 21 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP20/21. The complete amino acid sequence corresponds to amino acids 1 to 432 of SEQ ID NO:116. Underlined are the partially characterized N-terminal predicted partial amino acid (SEQ ID NO:50) sequence and the partially characterized C-terminal amino predicted partial acid (SEQ ID NO: 87) sequence. Indicated are further differences in amino acid sequence between SEQ ID NO:87 and SEQ ID NO:116.

Figure 22 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP22. The complete nucleotide sequence corresponds to nucleic acids 1 to 1977 of SEQ ID NO:51. Underlined is the partially characterized nucleotide (SEQ ID NO:22). Indicated are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP22 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 23 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP22. The complete amino acid sequence corresponds to amino acids 1 to 559 of SEQ ID NO:117. Underlined is the predicted partial amino acid (SEQ ID NO:88) sequence.

Figure 24 depicts the cDNA sequence and predicted amino acid sequence of the
5 *Arabidopsis thaliana* CCP23. The complete nucleotide sequence (Figure 24A) corresponds to nucleic acids 1 to 525 of SEQ ID NO:52. Indicated in Figure 24A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP23 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID
10 NOs:23 and SEQ ID NO:52 are depicted. The amino acid sequence in Figure 24B corresponds to amino acids 1 to 98 of SEQ ID NO:89. The complete amino acid sequence in Figure 24C corresponds to amino acids 1 to 86 of SEQ ID NO:118.

Figure 25 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP24. The complete nucleotide sequence corresponds to nucleic acids 1 to 2610 of SEQ ID NO:53.
15 Underlined is the partially characterized nucleotide (SEQ ID NO:24). Indicated are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP24 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 26 depicts the predicted amino acid sequence of the *Arabidopsis thaliana*
20 CCP24. The complete amino acid sequence corresponds to amino acids 1 to 784 of SEQ ID NO:119. Underlined is the predicted partial amino acid (SEQ ID NO:90) sequence.

Figure 27 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP25. The complete nucleotide sequence corresponds to nucleic acids 1 to 2235 of SEQ ID NO:54. Underlined is the partially characterized nucleotide (SEQ ID NO:25) sequence. Indicated
25 are stop and start codon (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP25 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 28 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP25. The complete amino acid sequence corresponds to amino acids 1 to 724 of SEQ
30 ID NO:120. Underlined is the predicted partial amino acid (SEQ ID NO:91) sequence.

Figure 29 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP26. The complete nucleotide sequence corresponds to nucleic acids 1 to 4002 of SEQ ID NO:55.

Underlined is the partially characterized nucleotide (SEQ ID NO:26) sequence. Indicated are stop and start codon (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP26 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID
5 NOs:26 and SEQ ID NO:55 are depicted.

Figure 30 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP26. The complete amino acid sequence corresponds to amino acids 1 to 1313 of SEQ ID NO:121. Underlined is the predicted partial amino acid (SEQ ID NO:92) sequence. Amino acid sequence differences between SEQ ID NOs:92 and SEQ ID NO:121 are
10 depicted.

Figure 31 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP27. The complete nucleotide sequence (Figure 31A) corresponds to nucleic acids 1 to 1251 of SEQ ID NO:56. The complete amino acid sequence (Figure 31B) corresponds to amino acids 1 to 310 of SEQ ID NO:122.
15 Underlined in Figure 31A and Figure 31B are the partially characterized nucleotide (SEQ ID NO:27) and predicted partial amino acid (SEQ ID NO:93) sequence, respectively. Indicated in Figure 31A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP27 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence
20 differences between SEQ ID NO:27 and SEQ ID NO:56 are depicted in Figure 31A.

Figure 32 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP28. The complete nucleotide sequence corresponds to nucleic acids 1 to 2955 of SEQ ID NO:56. Underlined is the partially characterized nucleotide (SEQ ID NO:28) sequence. Indicated are the stop and start codons (both in black shaded boxes) which are part of the primers
25 (grey shaded boxes) used to amplify the coding region of CCP28 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:28 and SEQ ID NO:57 are depicted.

Figure 33 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP28. The complete amino acid sequence corresponds to amino acids 1 to 964 of SEQ
30 ID NO:123. Underlined is the predicted partial amino acid (SEQ ID NO:94) sequence.

Figure 34 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP29. The complete nucleotide sequence (Figure 34A)

corresponds to nucleic acids 1 to 546 of SEQ ID NO:29. The complete amino acid sequence (Figure 34B) corresponds to amino acids 1 to 181 of SEQ ID NO:95. Indicated in Figure 34A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP29 by PCR. SEQ ID
5 NOs of the primers used can be found in Table III.

Figure 35 depicts the cDNA sequences and predicted amino acid sequences of the *Arabidopsis thaliana* CCP30. The complete nucleotide sequence (Figure 35A) corresponds to nucleic acids 1 to 492 of SEQ ID NO:30. Indicated in Figure 35A are the stop and start codons (both in black shaded boxes), the complete sense primer and part of
10 the antisense primer (grey shaded boxes) used to amplify the coding region of CCP30 by PCR. SEQ ID NOs of the primers used can be found in Table III. However, after sequencing of the PCR product a sequence error in SEQ ID NO:30 was detected (boxed nucleotide 'a' in Figure 35A not present) which caused a frame shift effectuating the CCP30 open reading frame. The putative correct cDNA sequence is given in Figure 35B
15 (nucleic acids 1 to 865 of SEQ ID NO:58) wherein the three putative start codons are marked by a black shaded box. The originally identified start codon is indicated in bold letters. The stop codon is unaltered. The amino acid sequence in Figure 35C corresponds to amino acids 1 to 163 of SEQ ID NO:96, the protein encoded by the initially identified open reading frame of SEQ ID NO:30. The putative correct complete amino acid sequence
20 in Figure 35D corresponds to amino acids 1 to 222 of SEQ ID NO:124 which comprises the longest possible open reading frame. The Met residues corresponding to the three possible start codons in SEQ ID NO:58 (Figure 35B) are bold faced.

Figure 36 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP31. The complete nucleotide sequence corresponds to nucleic acids 1 to 723 of SEQ ID NO:31.
25 Indicated in Figure 1A are the stop and start codons (both in black shaded boxes).

Figure 37 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP31. The complete amino acid sequence corresponds to amino acids 1 to 148 of SEQ ID NO:125.

Figure 38 depicts the cDNA sequence and predicted amino acid sequence of the
30 *Arabidopsis thaliana* CCP32. The complete nucleotide sequence (Figure 38A) corresponds to nucleic acids 1 to 426 of SEQ ID NO:60. The complete amino acid sequence (Figure 38B) corresponds to amino acids 1 to 70 of SEQ ID NO:126. Underlined

in Figure 38A is the partially characterized nucleotide (SEQ ID NO:32) sequence.

Indicated in Figure 38A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP32 by PCR. SEQ ID NOs of the primers used can be found in Table III. Figure 38C gives the
5 originally erroneously predicted amino acid sequence of CCP32 (amino acids 1 to 38 of SEQ ID NO:98).

Figure 39 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP33. The complete nucleotide sequence (Figure 39A)

corresponds to nucleic acids 1 to 1442 of SEQ ID NO:61. The complete amino acid

10 sequence (Figure 39B) corresponds to amino acids 1 to 385 of SEQ ID NO:127. Indicated in Figure 39A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP33 by PCR. SEQ ID NOs of the primers used can be found in Table III. Indicated in Figure 39B are the DNA binding domain (black shaded box), DEF domain (grey shaded box), DCB1 domain
15 (single underlined) and DCB2 domain (double underlined), all domains characteristic for a DP protein.

Figure 40 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP34. The complete nucleotide sequence (Figure 40A)

corresponds to nucleic acids 1 to 1506 of SEQ ID NO:62. The complete amino acid

20 sequence (Figure 40B) corresponds to amino acids 1 to 437 of SEQ ID NO:128.

Underlined in Figure 40A and Figure 40B are the partially characterized nucleotide (SEQ ID NO:34) and predicted partial amino acid (SEQ ID NO:62) sequence, respectively.

Indicated in Figure 40A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP34 by

25 PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 41 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP35. The complete nucleotide sequence corresponds to nucleic acids 1 to 2631 of SEQ ID NO:63.

Underlined is the partially characterized nucleotide (SEQ ID NO:35) sequence. Indicated are the stop and start codons (both in black shaded boxes) and of the primers (grey shaded

30 boxes) used to amplify the coding region of CCP35 by PCR. SEQ ID NOs of the primers used can be found in Table III. Nucleotide sequence differences between SEQ ID NO:33 and SEQ ID NO:63 are depicted.

Figure 42 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP35. The complete amino acid sequence corresponds to amino acids 1 to 749 of SEQ ID NO:129. Underlined is the predicted partial amino acid (SEQ ID NO:101) sequence.

Figure 43 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP36. The complete nucleotide sequence corresponds to nucleic acids 1 to 2743 of SEQ ID NO:64. Underlined is the partially characterized nucleotide (SEQ ID NO:36) sequence. Indicated are the stop and start codons (both in black shaded boxes). Nucleotide sequence differences between SEQ ID NO:36 and SEQ ID NO:64 are depicted.

Figure 44 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP36. The complete amino acid sequence corresponds to amino acids 1 to 742 of SEQ ID NO:130. Underlined is the predicted partial amino acid (SEQ ID NO:102) sequence.

Figure 45 depicts the cDNA sequence of the *Arabidopsis thaliana* CCP37. The complete nucleotide sequence corresponds to nucleic acids 1 to 2959 of SEQ ID NO:65. Underlined is the partially characterized nucleotide (SEQ ID NO:37) sequence. Indicated are the stop and start codons (both in black shaded boxes) and primers (grey shaded boxes) used to amplify the coding region of CCP45 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 46 depicts the predicted amino acid sequence of the *Arabidopsis thaliana* CCP37. The complete amino acid sequence corresponds to amino acids 1 to 911 of SEQ ID NO:131. Underlined is the predicted partial amino acid (SEQ ID NO:103) sequence. Indicated in a black shaded box is a SAP-like domain.

Figure 47 depicts the cDNA sequence and predicted amino acid sequence of the *Arabidopsis thaliana* CCP38. The complete nucleotide sequence (Figure 47A) corresponds to nucleic acids 1 to 1295 of SEQ ID NO:66. The complete amino acid sequence (Figure 47B) corresponds to amino acids 1 to 357 of SEQ ID NO:132. Underlined in Figure 47A and Figure 47B are the partially characterized nucleotide (SEQ ID NO:38) and predicted partial amino acid (SEQ ID NO:104) sequence, respectively. Indicated in Figure 47A are the stop and start codons (both in black shaded boxes) which are part of the primers (grey shaded boxes) used to amplify the coding region of CCP38 by PCR. SEQ ID NOs of the primers used can be found in Table III.

Figure 48 depicts phosphorylation of the *Arabidopsis thaliana* CCP4 by CDKs. The protein CDC2bDN-IC26M (SEQ ID NO:70) contains a consensus CDK

phosphorylation site (TPWK, residues 54-57 of SEQ ID NO:263). The corresponding gene (SEQ ID NO:4) was expressed in *E. coli* and the protein was purified from the crude extracts. The purified protein was subsequently shown to be phosphorylated by CDKs in an in vitro CDK phosphorylation assay. -: no IC26M added; +: IC26M added.

5 *Figure 49* schematically represents the domain organization of AtE2Fa and AtE2Fb. The DNA-binding domain (DB), the dimerization domain (DIM), the marked box (MB), and the Rb-binding domain (RB) are indicated by marked boxes, the N-terminal domains are indicated by open boxes. Numbering on the right refers to the amino acid sequence contained in the different AtE2F constructs, which were used in the in vitro
10 binding assays.

Figure 50 depicts AtDPa in vitro interactions with AtE2Fa and AtE2Fb. The *c-myc*-tagged AtDPa (*c-myc*-AtDPa) was in vitro translated and used as control. The lower migrating proteins observed in the case of *c-myc*-AtDPa are most probably due to initiation of translation at internal methionine codons (panel A, unnumbered left lane). The *c-myc*-
15 AtDPa was in vitro co-translated with HA-AtE2Fb (panels A and B, lane 1), HA-AtE2Fa (panels B, lane 2), the C-terminal deleted form of HA-AtE2Fb (panels A and B, lane 3), HA-AtE2Fa 1-420 (panels A and B, lane 4) and the N-terminal truncated form of HA-AtE2Fa 162-485 (panels A and B, lane 5) as indicated. Numbers in the case of the mutant AtE2Fs refer to the amino acid sequence contained in these constructs (see Figure 49). An
20 aliquot of each sample was analyzed directly by SDS-PAGE and autoradiographed (panel A; total IVT, total in vitro translation). Another aliquot of the same samples was subjected to immunoprecipitation with anti-*c-myc* monoclonal antibodies (panel B), lanes are indicated by numbering. The position of *c-myc*-AtDPa proteins are marked by arrows in both panels. Molecular mass markers are indicated at the left.

25 *Figure 51* shows AtDPb in vitro interactions with AtE2Fa and AtE2Fb. The *c-myc*-tagged AtDPb (*c-myc*-AtDPb, panels A and B, lane 2) and the HA-tagged AtE2Fb (HA-AtE2Fb, panels A and B, lane 1) were in vitro translated and used as controls. The lower migrating proteins observed in the case of *c-myc*-AtDPb are most probably due to initiation of translation at internal methionine codons (panel A, lane 2). The *c-myc*-AtDPb was in
30 vitro co-translated with HA-AtE2Fb (panels A and B, lane 3), HA-AtE2Fa (panels A and B lane 4), HA-AtE2Fa 1-420 (panels A and B, lane 5) and the N-terminal truncated form of HA-AtE2Fa 162-485 (panels A and B, lane 6) as indicated. Numbers in the case of the

mutant AtE2Fs refer to the amino acid sequence contained in these constructs (see Figure 49). An aliquot of each sample was analyzed directly by SDS-PAGE and autoradiographed (panel A; total IVT, total in vitro translation). Another aliquot of the same samples was subjected to immunoprecipitation with anti-*c-myc* monoclonal antibodies (panel B), lanes are indicated by numbering. The *c-myc*-AtDPb (panels A and B, lanes 2-6; indicated with 'y') co-migrated almost exactly with the mutant HA-AtE2Fa 1-420 (panels A and B, lane 5; indicated with 'x') and HA-AtE2Fa 162-485 (panels A and B, lane 6; indicated with 'z') in the gel system. These polypeptides as well as the position of *c-myc*-AtDPa and *c-myc*-AtDPb proteins are marked by arrows marked with 'y', 'x' and 'z', respectively (cfr. *supra*). Molecular mass markers are indicated at the left.

Figure 52 schematically represents AtDPa and mutants. The DNA-binding domain (DB) and the dimerization domain (DIM) are indicated by marked boxes, N- and C-terminal regions are indicated by open boxes. Numbering on the right side refers to the amino acid sequence contained in the different AtDP constructs, which were used in the in vitro binding assays.

Figure 53 schematically represents AtDPb and mutants. The DNA-binding domain (DB) and the dimerization domain (DIM) are indicated by marked boxes, N- and C-terminal regions are indicated by open boxes. Numbering on the right side refers to the amino acid sequence contained in the different AtDP constructs, which were used in the in vitro binding assays.

Figure 54 shows the mapping of regions in AtDPa required for in vitro binding to AtE2Fb. HA-AtE2Fb was co-translated with series of *c-myc*-AtDPa mutants. An aliquot of each sample was analyzed directly by SDS-PAGE and autoradiographed (panel A). Another aliquot of the same samples was subjected to immunoprecipitation with anti-HA (panel B) or anti-*c-myc* (panel C) monoclonal antibodies. The *c-myc*-AtDPa mutants are marked by dots. Positions of the HA-AtE2Fb proteins are indicated by arrows. Molecular mass markers are indicated at the left.

Figure 55 shows the mapping of regions in AtDPb required for in vitro binding to AtE2Fb. HA-AtE2Fb was co-translated with series *c-myc*-AtDPb mutants. An aliquot of each sample was analyzed directly by SDS-PAGE and autoradiographed (panel A). Another aliquot of the same samples was subjected to immunoprecipitation with anti-HA (panel B) or anti-*c-myc* (panel C) monoclonal antibodies. The *c-myc*-AtDPb mutants are

marked by dots. Positions of the HA-AtE2Fb proteins are indicated by arrows. Molecular mass markers are indicated at the left.

Figure 56 shows the mapping of regions in AtDPb required for in vitro binding to AtE2Fb. HA-AtE2Fb was co-translated with *c-myc*-AtDPb 182-263. Because of the small size of this protein, it was hardly detectable when it was directly analyzed by SDS-PAGE (data not shown). An aliquot of this sample was subjected to immunoprecipitation with *anti-c-myc* monoclonal antibodies. The *c-myc*-AtDP mutant is marked by dots. Position of the HA-AtE2Fb protein is indicated by an arrow. Molecular mass markers are indicated at the left.

Figure 57 shows organ- and cell cycle-specific expression of AtE2Fa and AtDPa. Tissue-specific expression of AtDPa and AtE2Fa genes. cDNA prepared from the indicated tissues was subjected to semi-quantitative RT-PCR analysis. The *Arath*;CDKB1;1 gene was used as a marker for highly proliferating tissues. The actin 2 gene (ACT2) was used as loading control.

Figure 58 shows organ- and cell cycle-specific expression of AtE2Fa and AtDPa. Co-regulated cell cycle phase-dependent transcription of AtE2Fa and AtDPa. The cDNA was prepared from partially synchronized *Arabidopsis* cells harvested at the indicated time point after removal of the cell cycle blocker was subjected to semi-quantitative RT-PCR analysis. Histone H4 and *Arath*;CDKB1;1 were used as markers for S and G2/M phase, respectively, and ROC5 and *Arath*;CDKA;1 as loading controls.

Figure 59 is a photographic representation of Northern blotting analysis of DPa expression in independent *Arabidopsis thaliana* DPa overexpressing lines (lines 16-27 as indicated) and one untransformed control line (indicated by C).

Figure 60 describes the molecules defined in SEQ ID NOs:199-204 and 240-290.

25 **Detailed Description of the Invention**

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as "cell cycle proteins" or "CCP" nucleic acid and polypeptide molecules. The CCP molecules of the present invention were identified based on their ability, as determined using yeast two-hybrid assays (described in detail in Example 1), to interact with proteins involved in the cell cycle, such as plant cyclin dependent kinases (e.g., a dominant negative form of CDC2b, CDC2bAt.N161), cyclin dependent kinase subunits referred herein as "CKS" (such as CKS1At), cyclin dependent kinase inhibitors

referred to herein as "CKI" (such as CKI4), PHO80-like proteins referred to herein as "PLP", E2F, and different domains of kinesin-like proteins referred to herein as "KLPNT.

Because of their ability to interact with (*e.g.*, bind to) the cyclin dependent kinases, the CCP molecules of the present invention may modulate, *e.g.*, upregulate or downregulate, the activity of plant CDKs, such as CDC2a or CDC2b; CKSs, CKIs, PLPs and KLPNTs. Furthermore, because of their ability to interact with (*e.g.*, bind to) the aforementioned proteins which are proteins involved in cell cycle regulation, the CCP molecules of the present invention may also play a role in or function in cell cycle regulation, *e.g.*, plant or animal cell cycle regulation.

As used herein, the term "cell cycle protein" includes a polypeptide which is involved in controlling or regulating the cell cycle, or part thereof, in a cell, tissue, organ or whole organism. Cell cycle proteins may also be capable of binding to, regulating, or being regulated by cyclin dependent kinases, such as plant cyclin dependent kinases, *e.g.*, CDC2a or CDC2b, or their subunits. The term cell cycle protein also includes peptides, polypeptides, fragments, variant, homologs, alleles or precursors (*e.g.*, pre-proteins or pro-proteins) thereof.

As used herein, the term "cell cycle" includes the cyclic biochemical and structural events associated with growth, division and proliferation of cells, and in particular with the regulation of the replication of DNA and mitosis. The cell cycle is divided into periods called: G₀, Gap₁ (G₁), DNA synthesis (S), Gap₂ (G₂), and mitosis (M). Normally these four phases occur sequentially, however, the cell cycle also includes modified cycles wherein one or more phases are absent resulting in modified cell cycle such as endomitosis, acytokinesis, polyploidy, polyteny, and endoreduplication.

As used herein, the term "plant" includes reference to whole plants, plant organ (*e.g.*, leaves, stems, roots), plant tissue, seeds, and plant cells and progeny thereof. Plant cell, as used herein includes, without limitation, seeds, *e.g.*, seed suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores. The class of plants which can be used in the methods of the invention is generally as broad as the class of higher plants amenable of transformation techniques, including both monocotyledonous and dicotyledonous plants. Particularly preferred plants are *Arabidopsis thaliana*, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, cotton, sunflower or canola. The term plant also includes monocotyledonous (monocot) plants and dicotyledonous (dicot) plants including a fodder or forage legume, ornamental plant, food crop, tree, or shrub selected from the list comprising *Acacia spp.*, *Acer spp.*, *Actinidia spp.*, *Aesculus spp.*, *Agathis australis*, *Albizia amara*, *Alsophila tricolor*, *Andropogon spp.*, *Arachis spp.*, *Areca catechu*, *Astelia fragrans*, *Astragalus cicer*, *Baikiaea plurijuga*, *Betula spp.*, *Brassica spp.*, *Bruguiera gymnorrhiza*, *Burkea africana*, *Butea frondosa*, *Cadaba farinosa*, *Calliandra spp.*, *Camellia sinensis*,

Canna indica, *Capsicum* spp., *Cassia* spp., *Centroema pubescens*, *Chaenomeles*
spp., *Cinnamomum cassia*, *Coffea arabica*, *Colophospermum mopane*, *Coronillia varia*,
Cotoneaster serotina, *Crataegus* spp., *Cucumis* spp., *Cupressus* spp., *Cyathea dealbata*,
Cydonia oblonga, *Cryptomeria japonica*, *Cymbopogon* spp., *Cynthea dealbata*, *Cydonia*
5 *oblonga*, *Dalbergia monetaria*, *Davallia divaricata*, *Desmodium* spp., *Dicksonia squarosa*,
Diheteropogon amplexans, *Dioclea* spp., *Dolichos* spp., *Dorycnium rectum*, *Echinochloa*
pyramidalis, *Ehrartia* spp., *Eleusine coracana*, *Eragrostis* spp., *Erythrina* spp., *Eucalyptus*
spp., *Euclea schimperi*, *Eulalia villosa*, *Fagopyrum* spp., *Feijoa sellowiana*, *Fragaria* spp.,
Flemingia spp., *Freycinetia banksii*, *Geranium thunbergii*, *Ginkgo biloba*, *Glycine*
10 *javanica*, *Gliricidia* spp., *Gossypium hirsutum*, *Grevillea* spp., *Guibourtia coleosperma*,
Hedysarum spp., *Hemarthia altissima*, *Heteropogon contortus*, *Hordeum vulgare*,
Hyparrhenia rufa, *Hypericum erectum*, *Hyperthelia dissoluta*, *Indigo incarnata*, *Iris* spp.,
Leptarrhena pyrolifolia, *Lespediza* spp., *Lettuca* spp., *Leucaena leucocephala*, *Loudetia*
simplex, *Lotonus bainesii*, *Lotus* spp., *Macrotyloma axillare*, *Malus* spp., *Manihot*
15 *esculenta*, *Medicago sativa*, *Metasequoia glyptostroboides*, *Musa sapientum*, *Nicotianum*
spp., *Onobrychis* spp., *Ornithopus* spp., *Oryza* spp., *Peltophorum africanum*, *Pennisetum*
spp., *Persea gratissima*, *Petunia* spp., *Phaseolus* spp., *Phoenix canariensis*, *Phormium*
cookianum, *Photinia* spp., *Picea glauca*, *Pinus* spp., *Pisum sativum*, *Podocarpus totara*,
Pogonarthria fleckii, *Pogonarthria squarrosa*, *Populus* spp., *Prosopis cineraria*,
20 *Pseudotsuga menziesii*, *Pterolobium stellatum*, *Pyrus communis*, *Quercus* spp.,
Raphiolepis umbellata, *Rhopalostylis sapida*, *Rhus natalensis*, *Ribes grossularia*, *Ribes*
spp., *Robinia pseudoacacia*, *Rosa* spp., *Rubus* spp., *Salix* spp., *Schyzachyrium*
sanguineum, *Sciadopitys verticillata*, *Sequoia sempervirens*, *Sequoiadendron giganteum*,
Sorghum bicolor, *Spinacia* spp., *Sporobolus fimbriatus*, *Stiburus alopecuroides*,
25 *Stylosanthos humilis*, *Tadehagi* spp., *Taxodium distichum*, *Themeda triandra*, *Trifolium*
spp., *Triticum* spp., *Tsuga heterophylla*, *Vaccinium* spp., *Vicia* spp., *Vitis vinifera*, *Watsonia*
pyramidata, *Zantedeschia aethiopica*, *Zea mays*, amaranth, artichoke, asparagus, broccoli,
brussel sprout, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil,
oilseed rape, okra, onion, potato, rice, soybean, straw, sugarbeet, sugar cane, sunflower,
30 tomato, squash, and tea, amongst others, or the seeds of any plant specifically named
above or a tissue, cell or organ culture of any of the above species.

The cell cycle proteins of the present invention are involved in cell cycle regulation
 which is largely, but not completely, similar in plants and animals. Accordingly, the
 nucleic acid molecules and polypeptide of the invention, or derivatives thereof, may be
 35 used to modulate the cell cycle in a plant or an animal such as by modulating the activity
 or level or expression of CCP, altering the rate of the cell cycle or phases of the cell cycle,
 and entry into and out of the various cell cycle phases. In plants, the molecules of the
 present invention may be used in agriculture to, for example, improve the growth

characteristics of plant such as growth rate or size of specific tissues or organs, the architecture or morphology of the plant, increase crop yield, improve tolerance to environmental stress conditions (such as drought, salt, temperature, or nutrient deprivation), improve tolerance to plant pathogens that abuse the cell cycle or as targets to
 5 facilitate the identification of inhibitors or activators of CCPs that may be useful as phytopharmaceuticals such as herbicides or plant growth regulators.

As used herein, the term "cell cycle associated disorders" includes a disorder, disease or condition which is caused or characterized by a misregulation (*e.g.*, downregulation or upregulation), abuse, arrest, or modification of the cell cycle. In plants
 10 cell cycle associated disorders include endomitosis, acytokinesis, polyploidy, polyteny, and endoreduplication which may be caused by external factors such as pathogens (nematodes, viruses, fungi, or insects), chemicals, environmental stress (*e.g.*, drought, temperature, nutrients, or UV) resulting in for instance neoplastic tissue (*e.g.*, galls, root knots) or inhibition of cell division/proliferation (*e.g.*, stunted growth). Cell cycle
 15 associated disorders in animals include proliferative disorders or differentiative disorders, such as cancer, *e.g.*, melanoma, prostate cancer, cervical cancer, breast cancer, colon cancer, or sarcoma.

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as CCP protein and nucleic acid molecules, which comprise a family of
 20 molecules having certain conserved structural and functional features. The term "family" when referring to the protein and nucleic acid molecules of the invention is intended to mean two or more proteins or nucleic acid molecules having a common structural domain or motif and having sufficient amino acid or nucleotide sequence homology as defined herein. Such family members can be naturally or non-naturally occurring and can be from
 25 either the same or different species. For example, a family can contain a first protein of plant, *e.g.* *Arabidopsis*, origin, as well as other, distinct proteins of plant, *e.g.*, *Arabidopsis*, origin or alternatively, can contain homologues of other plants, *e.g.*, rice, or of non-plant origin. Members of a family may also have common functional characteristics.

In one embodiment of the invention, a CCP protein of the present invention is
 30 identified based on the presence of at least one or more of the following domains:

A. Cyclin destruction box

As used herein, the term "Cyclin destruction box" includes a domain of 9-10 amino acid residues in length which typically contains the following consensus pattern:

R - X₂ - L - X₂ - [I/V] - X₁₋₂ - N (SEQ ID NO:267),

35 wherein X can be any amino acid, X_n is a stretch of n Xs, X_{n-m} is a stretch of n to m Xs, and wherein [I/V] means that an Ile or Val residue can occur at that position. SEQ ID NO:267 depicts the minimal consensus sequence of the cyclin destruction box and

underlies the ubiquitin-mediated proteolytic destruction of the cyclins bearing this motif (Yamano *et al.* (1998), *EMBO J.* 17: 5670-5678; Renaudin *et al.* (1998) in Plant Cell Division (Francis, Dudits and Inzé, eds.), Portland Press Research Monograph, Portland Press Ltd. London (1998), pp 67-98).

5

B. Cyclin box motif 1

As used herein, the term "Cyclin box motif 1" includes a domain of 8 amino acid residues in length and which typically contains the following consensus pattern:

MRXIL[I/V]DW (SEQ ID NO:268),

- 10 wherein X can be any amino acid and wherein [I/V] means that an Ile or Val residue can occur at that position. This motif forms part of the helix H1 of the first cyclin fold and is the best conserved motif in the cyclinA/B family (Renaudin *et al.* (1998) in Plant Cell Division (Francis, Dudits and Inzé, eds.), Portland Press Research Monograph, Portland Press Ltd. London (1998), pp 67-98).

15

C. Cyclin box motif 2

As used herein, the term "Cyclin box motif 2" includes a domain of 8 amino acid residues in length and which typically contains the following consensus pattern:

KYEE - X₃ - P (SEQ ID NO:269),

- 20 wherein X can be any amino acid and wherein X_n is a stretch of n Xs. This motif forms part of the helix H3 of the first cyclin fold wherein the 2 acidic residues are part of the CDK binding site (Renaudin *et al.* (1998) in Plant Cell Division (Francis, Dudits and Inzé, eds.), Portland Press Research Monograph, Portland Press Ltd. London (1998), pp 67-98).

25 D. CDC2 motifs

As used herein, the term "CDC2 motifs" includes domains of about 9-12 amino acid residues in length and which typically contain one of the following consensus patterns:

GXG -X₂- GXVY (SEQ ID NO:270)

30

HRDXK-X₂- NXL (SEQ ID NO:271)

D-X₁₋₂-[W/Y]SXG -X₄- E (SEQ ID NO:272)

wherein wherein X can be any amino acid, X_n is a stretch of n Xs, X_{n-m} is a stretch of n to m Xs, and wherein [W/Y] means that an Trp or Tyr residue can occur at that position.

35

E. CDK phosphorylation site

As used herein the term "CDK phosphorylation site" includes a domain of about 5-7 amino acids in length and which contains one or more of the following consensus domains:

- 5 TPX₁₋₂[R/K] (SEQ ID NO:273)
 SPX[R/K] (SEQ ID NO:274)
 SPX(Hu) (SEQ ID NO:275)
 SP(Hu)X (SEQ ID NO:276)

10 with Hu being a hydrophobic uncharged amino acid (M, I, L, V) and X any amino acid. The foregoing are typically found in cyclin-dependent kinase substrates such as histone kinase, transcription factors such as E2F or transcription regulators like Rb. CDK phosphorylation sites are described in, for example, Tamrakar *et al.* 2000, *Frontiers Biosci* 5, d121-137.

15 CCP proteins of the present invention comprising a CDK phosphorylation site can be mutated in said CDK phosphorylation site such that said CCP proteins are no longer able to be phosphorylated on the CDK phosphorylation site. Mutations of a CDK phosphorylation site include all mutations of the ser or thr residue in any of SEQ ID NOs:273-276 into a non-phosphorylatable amino acid residue, *e.g.*, an ala or glu residue.
 20 Mutation of one or more CDK phosphorylation site(s) in a CCP protein of the invention is expected to modulate modifications of the CCP protein by CDKs and, thus, to modulate the biological or biochemical function of the CCP protein.

F. E Nuclear localisation signal (NLS)

25 As used herein the term "nuclear localization signal" or "NLS" includes a domain conferring to a protein comprising the NLS domain the ability to be imported into the nucleus and to, for example, accumulate within the nucleus. NLS domains include one or more of the following concensus patterns:

- 30 PKKKRKV (SEQ ID NO:277)
 KRX₁₀KKKK (SEQ ID NO:278)
 KRPRP (SEQ ID NO:279)
 PAAKRVKLD (SEQ ID NO:280)

35 NLS domains have been found in the SV40 T antigen, in nucleoplasmin (bipartite NLS), in a Adeno E1A, and in c-Myc. NLS domains are described in, for example, Laskey *et al.* (1998) *Biochem. Soc. Trans.* 26, 561-567.

G. Cy-like boxes

As used herein, the term "Cy-like box" includes a domain of 3-6 amino acid residues in length with has the consensus motif R-X-X-F (SEQ ID NO:281) with X being any amino acid and one of two Xs preferably being a hydrophobic residue.

H. Rb binding domain

As used herein, the term "Rb binding domain" includes a domain which when present in a protein confers to the protein the ability to bind the Rb protein. Rb binding domains include one or more of the following consensus patterns:

LXCXE (SEQ ID NO:282)

LXSXE (SEQ ID NO:283)

DYX₇EX₃DLFD (SEQ ID NO:284)

DYX₆DX₄DMWE (SEQ ID NO:285)

Rb binding domains have been found in D-cyclins, in protein phosphatase 1, in human E2F-1, and in plant E2F. Rb binding domains are described in, for example, Rubin *et al.* (1998) *Frontiers Biosci* 3, d1209-1219; Phelps *et al.* (1992) *J. Virol.* 66, 2418-2427, and Cress *et al.* (1993) *Mol. Cell Biol.* 13, 6314-6325.

I. DEF Domain

As used herein the term "DEF domain" includes a protein domain which is required for the formation of heterodimers between DP proteins and E2F proteins. DEF domains comprise the following consensus pattern:

[D/N/-][Q/E]KNIR[R/G]RV[Y/D]DALNV[L/F]MA[M/I/L/-][N/D]
[V/I][S/A][K/R][D/E]KKEI[K/Q/R/-]W[R/K/T]GLP
(SEQ ID NO:286)

J. DNA Binding Domain

As used herein the term "DNA binding domain" includes a domain which is involved in the binding of DP proteins and/or DP-E2F heterodimers to DNA. DNA binding domains include the following consensus pattern:

[G/N][K/R]GLR[H/Q]FS[M/V][K/M][I/V]X₍₀₋₁₇₎C[E/Q]K[V/L][Q/E/-][S/-]XK[G/K]-
[R/I/-]TT[S/-]Y[N/K]EVADE[L/T][V/I][A/S][E/D]F
(SEQ ID NO:287)

DNA binding domains are described in, for example, Hao *et al.* (1995) *J. Cell Sci.* 108, 2945-2954; Bandara *et al.* (1993) *EMBO J.* 12, 4317-4324; and Girling *et al.* (1994) *Mol. Biol. Cell* 5, 1081-1092.

5 K. DCB1 Domain:

As used herein the term "DCB1 domain" includes a protein domain which is conserved among DP proteins and has the following consensus patterns:

[R/S][I/V]X[Q/K]KX₃[L/S]XE
 (SEQ ID NO:288)
 10 [R/S][I/V]X[Q/K]KX₃[L/S]XE[L/M]X_{2,3}[Q/H]X_{4,5}NL[V/I/M][Q/E]RN
 (SEQ ID NO:289)

DCB1 domains are described in, for example, Hao *et al.* (1995) *J. Cell Sci.* 108, 2945-
 15 2954; Bandara *et al.* (1993) *EMBO J.* 12, 4317-4324; and Girling *et al.* (1994) *Mol. Biol. Cell* 5, 1081-1092.

L. DCB2 Domain:

As used herein the term "DCB2 domain" includes a protein domain which is
 20 conserved among DP proteins and has the following consensus pattern:

[L/I]PFI[L/I][V/L]XTX_{3,4}[T/V]VX₁₂₋₁₄FX_{3,4}F[E/S][Hu]HDDX₂[V/I]L[R/K]XM
 (SEQ ID NO:290)

DCB2 domains are described in, for example, Hao *et al.* (1995) *J. Cell Sci.* 108, 2945-
 25 2954; Bandara *et al.* (1993) *EMBO J.* 12, 4317-4324; and Girling *et al.* (1994) *Mol. Biol. Cell* 5, 1081-1092.

M. SAP Domain:

30 As used herein the term SAP motif includes a protein domain of about 35 amino acid residues which is found in a variety of nuclear proteins involved in transcription, DNA repair, DNA processing or apoptotic chromatin degradation. It was named after SAF-A/B, Acinus and PIAS, three proteins known to contain it. The SAP motif reveals a bipartite distribution of strongly conserved hydrophobic, polar and bulky amino acids
 35 separated by a region that contains a glycine. The SAP domain has been proposed to be a DNA-binding motif (Aravind and Koonin (2000) *Trends Biochem. Sci.* 25:112-114).

Isolated CCP proteins of the present invention have an amino acid sequence sufficiently identical to the amino acid sequence of SEQ ID NO:67-132, 205, 211, 215-216, or 220-227 or are encoded by a nucleotide sequence sufficiently identical to SEQ ID NO:1-66 or 228-239. As used herein, the term "sufficiently identical" refers to a first amino acid or nucleotide sequence which contains a sufficient or minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences share common structural domains or motifs and/or a common functional activity. For example, amino acid or nucleotide sequences which share common structural domains have at least 30%, 40%, or 50% homology, preferably 60% homology, more preferably 70%-80%, and even more preferably 90-95% homology across the amino acid sequences of the domains and contain at least one and preferably two structural domains or motifs, are defined herein as sufficiently identical. Furthermore, amino acid or nucleotide sequences which share at least 30%, 40%, or 50%, preferably 60%, more preferably 70-80%, or 90-95% homology and share a common functional activity are defined herein as sufficiently identical.

As used interchangeably herein, an "CCP activity", "biological activity of CCP" or "functional activity of CCP", refers to an activity exerted by a CCP protein, polypeptide or nucleic acid molecule on a CCP responsive cell or tissue, or on a CCP protein substrate, as determined *in vivo*, or *in vitro*, according to standard techniques. In one embodiment, a CCP activity is a direct activity, such as an association with a CCP-target molecule. As used herein, a "target molecule" or "binding partner" is a molecule with which a CCP protein binds or interacts in nature, such that CCP-mediated function is achieved. A CCP target molecule can be a non-CCP molecule or a CCP protein or polypeptide of the present invention, *e.g.*, a plant cyclin dependent kinase, such as CDC2b. In an exemplary embodiment, a CCP target molecule is a CCP ligand. Alternatively, a CCP activity is an indirect activity, such as a cellular signaling activity mediated by interaction of the CCP protein with a CCP ligand. The biological activities of CCP are described herein. For example, the CCP proteins of the present invention can have one or more of the following activities: (1) they may interact with a non-CCP protein molecule, *e.g.*, a CCP ligand; (2) they may modulate a CCP-dependent signal transduction pathway; (3) they may modulate the activity of a plant cyclin dependent kinase, such as CDC2a, CDC2b, or CDC2c, and (4) they may modulate the cell cycle.

Accordingly, another embodiment of the invention features isolated CCP proteins and polypeptides having a CCP activity. Preferred proteins are CCP proteins having at least one or more of the following domains: a "cyclin destruction box", a "cyclin box motif 1", a "cyclin box motif 2", a "CDC2 motif", a "CDK phosphorylation site", a "nuclear localization signal", a "Cy-like box", an "Rb binding domain", a "DEF domain", a "DNA

-28-

binding domain", a "DCB1 domain", a "DCB2 domain" and/or a SAP domain, and, preferably, a CCP activity.

Additional preferred proteins have at least one or more of the following domains: a "cyclin destruction box", a "cyclin box motif 1", a "cyclin box motif 2", a "CDC2 motif",
 5 a "CDK phosphorylation site", a "nuclear localization signal", a "Cy-like box", an "Rb binding domain", a "DEF domain", a "DNA binding domain", a "DCB1 domain", a "DCB2 domain" and/or a SAP domain and are, preferably, encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID
 10 NO:1-66 or 228-239.

The sequences of the present invention are summarized below, in Table I.

TABLE I:

15

CCP Molecule	Clone Name	Bait	Homolog/ function	motif	SEQ ID NO: partial DNA	SEQ ID NO: full-length DNA	SEQ ID NO: partial Protein	SEQ ID NO: full-length Protein
CCP1	CDC2bD N-IC19	CDC2bAt. N161	Novel CYCB2;3	cyclin box motifs 1 and 2; cyclin destruction box	1	39	67	105
CCP2	CDC2bD N-IC20	CDC2bAt. N161	ARR2		2	40	68	106
CCP3	CDC2bD N-IC21	CDC2bAt. N161	novel A-type cyclin	cyclin box motifs 1 and 2; cyclin destruction box	3	41	69	107
CCP4	CDC2bD N-IC26M	CDC2bAt. N161		CDK phosphorylation site	4	4	70	70
CCP5	CDC2bD N-IC39	CDC2bAt. N161	ArathCYCB2 ;1	cyclin box motifs 1 and 2; cyclin	5	5	71	71

				destruction box				
CCP6	CDC2bD N-IC57	CDC2bAt. N161			6	42	72	108
CCP7	CDC2bD N-IC62	CDC2bAt. N161	AJH2-COP9		7	43	73	109
CCP8	E2F3ca55	E2F3 N- terminal			8	43	74	109
CCP9	CDC2bD N-IC9	CDC2bAt. N161	Arath CYCA2;2	cyclin box motifs 1 and 2; cyclin destruction box	9	9	75	75
CCP10	CKSBC0 01	CKS1At			10	10	76	76
CCP11	CKSBC0 11	CKS1At	gibberellin- regulated protein GASA1 precursor		11	44	77	110
CCP12	CKSBC9 8-7 (Cterm)	CKS1At			12	45	78	111
CCP13	CKSBC9 8-7 (Nterm)	CKS1At			13	45	79	111
CCP14	CKSBC1 03-19 (Cterm)	CKS1At			14	46	80	112
CCP15	CKSBC1 99-20	CKS1At	PSTTLRE-type CDK	CDC2 motifs	15	47	81	113
CCP16	E2F5BB C1	E2F5 dimerisati on domain	DPa	DNA-binding domain; DEF domain; DCB1 and DCB2 domain	16	48	82	114
CCP17	FL67BC4 -2	CKI4			17	17	83	83
CCP18	FL67BC1 2-17	CKI4	RNA polymerase B transcription factor 3		18	49	84	115
CCP19	JUT1	PLP1			19	19	85	85
CCP20	JUT2	PLP1			20	50	86	116
CCP21	JUT3	PLP1			21	50	87	116
CCP22	JUT6	PLP1	Submergence induced		22	51	88	117

-30-

			protein2 of Oryza sativa					
CCP23	kbp1	KLPNT1 36-508aa (motor domain) KLPNT2 (TH65) 73-186 aa (neck domain)	HSF1		23	52	89	118
CCP24	kbp3	KLPNT1 (427- 867aa) stalk domain			24	53	90	119
CCP25	kbp6	KLPNT2 (TH65) 73-186 aa neck domain			25	54	91	120
CCP26	kbp9	KLPNT2 (TH65) 73-186 aa neck domain	AtKLPNT1		26	55	92	121
CCP27	kbp11	KLPNT2 (TH65) 73-186 aa neck domain			27	56	93	122
CCP28	kbp12	KLPNT2 (TH65) 73-186 aa neck domain			28	57	94	123
CCP29	kbp13	KLPNT2 (TH65) 73-186 aa neck domain			29	29	95	95
CCP30	kbp15	KLPNT2 (TH65) 73-186 aa neck domain	Centromere/ microtubule binding protein CBF5 from yeast		30	58	96	124
CCP31	kbp20	KLPNT2	VU91C		31	59	97	125

-31-

		(TH65) 73-608 aa stalk domain	calmodulin from yeast					
CCP32	E2F5BB C16	E2F5 dimerizati on			32	60	98	126
CCP33	DPb	/		DNA-binding domain; DEF domain; DCB1 and DCB2 domain	33	61	99	127
CCP34	E2F3ca1	E2F3 N- terminal			34	62	100	128
CCP35	E2F3ca2	E2F3 N- terminal			35	63	101	129
CCP36	E2F3ca9	E2F3 N- terminal			36	64	102	130
CCP37	E2F3ca12	E2F3 N- terminal		SAP domain	37	65	103	131
CCP38	E2F3ca50	E2F3 N- terminal			38	66	104	132

Detailed studies of interactions between AtDPs (a and b forms, SEQ ID NO:114 and SEQ ID NO:127, respectively) and AtE2Fs (a and b forms; GenBank accession numbers AJ294534 and AJ294533, respectively) revealed that the regions of AtDPa and AtDPb involved in the binding of AtE2Fb are different.

Binding of AtDPa to AtE2Fb requires at least the AtDPa dimerization domain and the whole (or possibly part of) the C-terminal domain of AtDPa. The N-terminal domain and the DNA-binding domain of AtDPa do not seem to contribute to the interaction of AtDPa with AtE2Fb (Examples 11, 12, Table 5, Figure 54).

Binding of AtDPb to AtE2Fb, however, only requires an intact AtDPb dimerization domain. Neither the region including the N-terminal and DNA-binding domains of AtDPb, nor the C-terminal region of AtDPb seem to contribute to the interaction of AtDPb with AtE2Fb (Examples 11, 12, Table 5, Figure 55). These observations indicate that modulating the formation of specific E2F/DP-complexes may be useful in modulating cell cycle traversal and the regulation thereof.

AtDPa and AtDPb, respectively, do not form homodimers but both interact with either AtE2Fa or AtE2Fb (Example 12, Table 5). In reciprocal experiments it was shown that the N-terminal domain of AtE2Fa is not required for binding AtDPa or AtDPb. Likewise, the Rb-binding domains of AtE2Fa and AtE2Fb, respectively, do not seem to contribute to the binding to either AtDPa or AtDPb. The region of AtE2Fa encompassing

the dimerization domain and the marked box is sufficient for binding to AtDPa and AtDPb (Examples 11, 12, Fig. 50, Fig. 51, Table 5). The dimerization domain of AtE2Fs appears to be sufficient for binding to AtDPs.

- Accordingly, it is shown herein for the first time (for plant DP and plant E2Fs)
- 5 that the minimal DP and E2F proteins or corresponding coding DNA sequences that can be used in modifying E2F/DP-related processes, *e.g.*, regulation of gene expression by E2F/DP, include:

- (A) Plant DP dimerization domain with or without (part of) the C-terminal DP domain. These domains include the proteins AtDPa143-292 and AtDPa143-213
- 10 (numbering indicates the amino acids included in said fragment relative to the full-length AtDPa protein) set forth in SEQ ID NO:221 and SEQ ID NO:222, respectively. The coding sequences corresponding to the foregoing amino acid sequences are set forth in SEQ ID NO:232 and SEQ ID NO:233, respectively. Also included are the corresponding regions of the AtDPb protein characterized by AtDPb182-385 and AtDPb182-263 (parts of
- 15 the full-length AtDPb protein). The foregoing regions of AtDPb are set forth in SEQ ID NO:216 and SEQ ID NO:215, respectively, and the coding sequences corresponding thereto are set forth in SEQ ID NO:231 and SEQ ID NO:230, respectively. The AtDPb1-263 domain (SEQ ID NO:223) and the corresponding AtDPa1-214 domain (SEQ ID NO:220) encoded by the nucleic acid sequences SEQ ID NO:234 and SEQ ID NO:239,
- 20 respectively, can also be used. Further included are nucleic acid sequences hybridizing to SEQ ID NOs:229-234 or SEQ ID NO:239 or encoding a protein at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more identical to SEQ ID NOs:211, 215-216 and 220-223.

- (B) Plant E2F dimerization domain with or without (part of) the marked box.
- 25 These domains include the proteins AtE2Fa232-282, AtE2Fa232-352 and AtE2Fa226-356 set forth in SEQ ID NO:224, SEQ ID NO:225 and SEQ ID NO:205, respectively. The corresponding coding DNA sequences are set forth in SEQ ID NO:235, SEQ ID NO:236 and SEQ ID NO:228, respectively. Also included are the corresponding regions of the AtE2Fb protein characterized by AtE2Fb194-243 and AtE2Fb194-311 set forth in SEQ ID
- 30 NO:226 and SEQ ID NO:227, respectively. The corresponding coding DNA sequences are set forth in SEQ ID NO:237 and SEQ ID NO:238, respectively. Further included are nucleic acid sequences hybridizing to SEQ ID NO:228 or SEQ ID NOs:235-238 or encoding a protein at least 70%, 75%, 80%, 85%, 90%, 95%, 98% identical to SEQ ID NO:205 or SEQ ID NOs:224-227.

- 35 (C) Full-length plant DP and plant E2F proteins or corresponding DNA sequences may also be used to modify said E2F/DP-related processes. Furthermore, plant DP and plant E2F proteins or corresponding DNA sequences, or parts thereof, can be used either separately or in combination to modify said E2F/DP-related processes. This is underscored

by the demonstration that AtDPs and AtE2Fs are co-expressed in actively dividing cells and in at least some plant tissues (Example 13 and Figures 57 and 58).

Various aspects of the invention are described in further detail in the following
5 subsections:

I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode CCP proteins or biologically active portions thereof, as well as nucleic acid fragments
10 sufficient for use as hybridization probes to identify CCP-encoding nucleic acids (*e.g.*, CCP mRNA) and fragments for use as PCR primers for the amplification or mutation of CCP nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic
15 acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. For example, with regards to genomic DNA, the term "isolated" includes nucleic acid molecules which
20 are separated from the chromosome with which the genomic DNA is naturally associated. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated CCP nucleic acid molecule can contain less than about 5 kb,
25 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals
30 when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:1-66 or 228-239, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, using all or portion of the nucleic acid sequence of SEQ ID
35 NO:1-66 or 228-239, as a hybridization probe, CCP nucleic acid molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold

Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

Moreover, a nucleic acid molecule encompassing all or a portion of SEQ ID NO:1-66 or 228-239 can be isolated by the polymerase chain reaction (PCR) using synthetic oligonucleotide primers designed based upon the sequence of SEQ ID NO:1-66 or 228-239, respectively.

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to CCP nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239, or a portion of any of these nucleotide sequences. A nucleic acid molecule which is complementary to the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239, is one which is sufficiently complementary to the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239, respectively, such that it can hybridize to the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239, respectively, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the present invention comprises a nucleotide sequence which is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more homologous to the nucleotide sequence (*e.g.*, to the entire length of the nucleotide sequence) shown in SEQ ID NO:1-66 or 228-239, or a portion of any of these nucleotide sequences.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the nucleic acid sequence of SEQ ID NO:1-66 or 228-239, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of a CCP protein. The nucleotide sequence determined from the cloning of the CCP gene allows for the generation of probes and primers designed for use in identifying and/or cloning other CCP family members, as well as CCP homologues from other species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12 or 15, preferably about 20 or 25, more preferably about 30, 35, 40, 45, 50, 55, 60, 65, or 75 consecutive nucleotides of a sense sequence of SEQ ID NO:1-66 or 228-239, or of a naturally occurring allelic variant or mutant of SEQ

ID NO:1-66 or 228-239. In an exemplary embodiment, a nucleic acid molecule of the present invention comprises a nucleotide sequence which is at least 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, or 800 nucleotides in length and hybridizes under stringent hybridization conditions to a nucleic acid molecule of SEQ ID
5 NO:1-66 or 228-239.

Probes based on the CCP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes
10 can be used as a part of a diagnostic test kit for identifying cells or tissues which misexpress a CCP protein, such as by measuring a level of a CCP-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting CCP mRNA levels or determining whether a genomic CCP gene has been mutated or deleted.

A nucleic acid fragment encoding a "biologically active portion of a CCP protein"
15 can be prepared by isolating a portion of the nucleotide sequence of SEQ ID NO:1-66 or 228-239, which encodes a polypeptide having a CCP biological activity (the biological activities of the CCP proteins are described herein), expressing the encoded portion of the CCP protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the CCP protein.

20 The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239, due to the degeneracy of the genetic code and, thus, encode the same CCP proteins as those encoded by the nucleotide sequence shown in SEQ ID NO:1-66 or 228-239. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a CCP protein.

25 In addition to the CCP nucleotide sequences shown in SEQ ID NO:1-66 or 228-239, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the CCP proteins may exist within a population (*e.g.*, an *Arabidopsis* or rice plant population). Such genetic polymorphism in the CCP genes may exist among individuals within a population due to natural allelic
30 variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules which include an open reading frame encoding an CCP protein, preferably a plant CCP protein, and can further include non-coding regulatory sequences, and introns. Such natural allelic variations include both functional and non-functional CCP proteins and can typically result in 1-5% variance in the nucleotide sequence of a CCP gene. Any
35 and all such nucleotide variations and resulting amino acid polymorphisms in CCP genes

that are the result of natural allelic variation and that do not alter the functional activity of a CCP protein are intended to be within the scope of the invention. Differences in preferred codon usage are illustrated below for *Agrobacterium tumefaciens* (a bacterium), *Arabidopsis thaliana*, *Medicago sativa* (two dicotyledonous plants) and *Oryza sativa* (a monocotyledonous plant). These examples were extracted from <http://www.kazusa.or.jp/codon>. For example, the codon GGC (for glycine) is the most frequently used codon in *A. tumefaciens* (36.2 %), is the second most frequently used codon in *O. sativa* but is used at much lower frequencies in *A. thaliana* and *M. sativa* (9 % and 8.4 % , respectively). Of the four possible codons encoding glycine the GGC codon is most preferably used in *A. tumefaciens* and *O. sativa*. However, in *A. thaliana* the GGA (and GGU) codon is most preferably used, whereas in *M. sativa* the GGU (and GGA) codon is most preferably used.

Moreover, nucleic acid molecules encoding other CCP family members and, thus, which have a nucleotide sequence which differs from the CCP sequences of SEQ ID NO:1-66 or 228-239 are intended to be within the scope of the invention. For example, another CCP cDNA can be identified based on the nucleotide sequence of the plant CCP molecules described herein. Moreover, nucleic acid molecules encoding CCP proteins from different species, and thus which have a nucleotide sequence which differs from the CCP sequences of SEQ ID NO:1-66 or 228-239 are intended to be within the scope of the invention. For example, a human CCP cDNA can be identified based on the nucleotide sequence of a plant CCP.

Nucleic acid molecules corresponding to natural allelic variants and homologues of the CCP cDNAs of the invention can be isolated based on their homology to the CCP nucleic acids disclosed herein using the cDNAs disclosed herein, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15, 20, 25, 30 or more nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-66 or 228-239. In other embodiment, the nucleic acid is at least 30, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, or 600 nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 30%, 40%, 50%, or 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 70%, more preferably at least about 80%, even more preferably at least about 85% or 90% homologous to each other typically

acid. The antisense nucleic acid can be complementary to an entire CCP coding strand, or only to a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding CCP. The term "coding region" refers to the region of the nucleotide sequence comprising
5 codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding CCP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

10 Given the coding strand sequences encoding CCP disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of CCP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of CCP mRNA. For example, the
15 antisense oligonucleotide can be complementary to the region surrounding the translation start site of CCP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an
20 antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used
25 to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine,
30 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-
35 oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted

nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection). Preferably, production of antisense nucleic acids in plants occurs by means of a stably integrated transgene comprising a promoter operative in plants, an antisense oligonucleotide, and a terminator.

5 Other known nucleotide modifications include methylation, cyclization and 'caps' and substitution of one or more of the naturally occurring nucleotides with an analog such as inosine. Modifications of nucleotides include modifications generated by the addition to nucleotides of acridine, amine, biotin, cascade blue, cholesterol, Cy3[®], Cy5[®], Cy5.5[®] Dabcyl, digoxigenin, dinitrophenyl, Edans, 6-FAM, fluorescein, 3'-glyceryl, HEX, IRD-
10 700, IRD-800, JOE, phosphate psoralen, rhodamine, ROX, thiol (SH), spacers, TAMRA, TET, AMCA-S[®], SE, BODIPY[®], Marina Blue[®], Pacific Blue[®], Oregon Green[®], Rhodamine Green[®], Rhodamine Red[®], Rhodol Green[®] and Texas Red[®]. Polynucleotide backbone modifications include methylphosphonate, 2'-OMe-methylphosphonate RNA, phosphorothiorate, RNA, 2'-OMeRNA. Base modifications include 2-amino-dA, 2-
15 aminopurine, 3'-(ddA), 3'dA(cordycepin), 7-deaza-dA, 8-Br-dA, 8-oxo-dA, N⁶-Me-dA, abasic site (dSpacer), biotin dT, 2'-OMe-5Me-C, 2'-OMe-propynyl-C, 3'-(5-Me-dC), 3'-(ddC), 5-Br-dC, 5-I-dC, 5-Me-dC, 5-F-dC, carboxy-dT, convertible dA, convertible dC, convertible dG, convertible dT, convertible dU, 7-deaza-dG, 8-Br-dG, 8-oxo-dG, O⁶-Me-dG, S6-DNP-dG, 4-methyl-indole, 5-nitroindole, 2'-OMe-inosine, 2'-dI, O⁶-phenyl-dI, 4-
20 methyl-indole, 2'-deoxynebularine, 5-nitroindole, 2-aminopurine, dP(purine analogue), dK(pyrimidine analogue), 3-nitropyrrole, 2-thio-dT, 4-thio-dT, biotin-dT, carboxy-dT, O⁴-Me-dT, O⁴-triazol dT, 2'-OMe-propynyl-U, 5-Br-dU, 2'-dU, 5-F-dU, 5-I-dU, O⁴-triazol dU.

The antisense nucleic acid molecules of the invention are typically introduced into a plant or administered to a subject or generated *in situ* such that they hybridize with or
25 bind to cellular mRNA and/or genomic DNA encoding a CCP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. An
30 example of a route of introduction or administration of antisense nucleic acid molecules of the invention include transformation in a plant or direct injection at a tissue site in a subject. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or
35 antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules,

vector constructs in which the antisense nucleic acid molecule is placed under the control of a constitutive promoter or a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific
5 double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

10 In another embodiment, the antisense nucleic acid molecule further comprises a sense nucleic acid molecule complementary to the antisense nucleic acid molecule. Gene silencing methods based on such nucleic acid molecules are well known to the skilled artisan (*e.g.*, Grierson *et al.* (1998) WO 98/53083; Waterhouse *et al.* (1999) WO 99/53050).

15 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave
20 CCP mRNA transcripts to thereby inhibit translation of CCP mRNA. A ribozyme having specificity for a CCP-encoding nucleic acid can be designed based upon the nucleotide sequence of a CCP cDNA disclosed herein (*i.e.*, SEQ ID NO:1-66 or 228-239). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be
25 cleaved in a CCP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, CCP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

The use of ribozymes for gene silencing in plants is known in the art (*e.g.*, Atkins *et al.* (1994) WO 94/00012; Lenne *et al.* (1995) WO 95/03404; Lutziger *et al.* (2000) WO
30 00/00619; Prinsen *et al.* (1997) WO 97/13865 and Scott *et al.* (1997) WO/ 97/38116).

Alternatively, CCP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the CCP (*e.g.*, the CCP promoter and/or enhancers) to form triple helical structures that prevent transcription of the CCP
35 gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

In yet another embodiment, the CCP nucleic acid molecules of the present invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acid molecules can be modified to generate peptide nucleic acids (see Hyrup B. *et al.* (1996) *Bioorganic & Medicinal Chemistry* 4 (1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup B. *et al.* (1996) *supra*; Perry-O'Keefe *et al.* *Proc. Natl. Acad. Sci.* 93: 14670-675.

PNAs of CCP nucleic acid molecules can be used for increasing crop yield in plants or in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, for example, inducing transcription or translation arrest or inhibiting replication. PNAs of CCP nucleic acid molecules can also be used in the analysis of single base pair mutations in a gene, (*e.g.*, by PNA-directed PCR clamping); as 'artificial restriction enzymes' when used in combination with other enzymes, (*e.g.*, S1 nucleases (Hyrup B. (1996) *supra*)); or as probes or primers for DNA sequencing or hybridization (Hyrup B. *et al.* (1996) *supra*; Perry-O'Keefe *supra*).

In another embodiment, PNAs of CCP can be modified, (*e.g.*, to enhance their stability or cellular uptake), by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of CCP nucleic acid molecules can be generated which may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, (*e.g.*, RNase H and DNA polymerases), to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup B. (1996) *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup B. (1996) *supra* and Finn P.J. *et al.* (1996) *Nucleic Acids Res.* 24 (17): 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used as a between the PNA and the 5' end of DNA (Mag, M. *et al.* (1989) *Nucleic Acid Res.* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment

(Finn P.J. *et al.* (1996) *supra*). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser, K.H. *et al.* (1975) *Bioorganic Med. Chem. Lett.* 5: 1119-11124).

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.* (1989) *Proc. Natl. Acad. Sci. US.* 86:6553-6556; Lemaitre *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (See, *e.g.*, Krol *et al.* (1988) *Bio-Techniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon (1988) *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent).

15 II. Isolated CCP Proteins and Anti-CCP Antibodies

One aspect of the invention pertains to isolated CCP proteins (*e.g.*, the amino acid sequences set forth in SEQ ID NO:67-132, 205, 211, 215-216, or 220-227) and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise anti-CCP antibodies. In one embodiment, native CCP proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, CCP proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a CCP protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

25 An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the CCP protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of CCP protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of CCP protein having less than about 30% (by dry weight) of non-CCP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-CCP protein, still more preferably less than about 10% of non-CCP protein, and most preferably less than about 5% non-CCP protein. When the CCP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%,

more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of CCP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of CCP protein having less than about 30% (by dry weight) of chemical precursors or non-CCP chemicals, more preferably less than about 20% chemical precursors or non-CCP chemicals, still more preferably less than about 10% chemical precursors or non-CCP chemicals, and most preferably less than about 5% chemical precursors or non-CCP chemicals.

Biologically active portions of a CCP protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the CCP protein, which include less amino acids than the full length CCP proteins, and exhibit at least one activity of a CCP protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the CCP protein. A biologically active portion of a CCP protein can be a polypeptide which is, for example, at least 10, 25, 50, 100 or more amino acids in length.

To determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, or 90% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been

incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is
5 determined using the GAP program in the GCG software package (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A preferred, non-limiting example of parameters to be used in conjunction with the GAP program include a Blosum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of
10 5.

In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (*Comput. Appl. Biosci.*, 4:11-17 (1988)) which has been incorporated into the ALIGN program (version 2.0 or version 2.0U), using a PAM120 weight residue table, a gap length penalty of 12 and
15 a gap penalty of 4.

The nucleic acid and polypeptide sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.*
20 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to Kinase and Phosphatase nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 100, wordlength = 3, and a Blosum62 matrix to obtain amino acid sequences homologous to Kinase and Phosphatase polypeptide
25 molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

30 The invention also provides CCP chimeric or fusion proteins. As used herein, a CCP "chimeric protein" or "fusion protein" comprises a CCP polypeptide operatively linked to a non-CCP polypeptide. An "CCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to CCP, whereas a "non-CCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not
35 substantially homologous to the CCP protein, *e.g.*, a protein which is different from the CCP protein and which is derived from the same or a different organism. Within a CCP fusion protein the CCP polypeptide can correspond to all or a portion of a CCP protein. In a preferred embodiment, a CCP fusion protein comprises at least one biologically active

portion of a CCP protein. In another preferred embodiment, a CCP fusion protein comprises at least two biologically active portions of a CCP protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the CCP polypeptide and the non-CCP polypeptide are fused in-frame to each other. The non-CCP polypeptide can be fused to the N-terminus or C-terminus of the CCP polypeptide or can be inserted within the CCP polypeptide. The non-CCP polypeptide can, for example, be (histidine)₆-tag, glutathione S-transferase, protein A, maltose-binding protein, dihydrofolate reductase, Tag•100 epitope (EETARFQPGYRS; SEQ ID NO:199), c-myc epitope (EQKLISEEDL; SEQ ID NO:200), FLAG[®]-epitope (DYKDDDK; SEQ ID NO:201), lacZ, CMP (calmodulin-binding peptide), HA epitope (YPYDVPDYA; SEQ ID NO:202), protein C epitope (EDQVDPRLIDGK; SEQ ID NO:203) or VSV epitope (YTDIEMNRLGK; SEQ ID NO:204).

For example, in one embodiment, the fusion protein is a GST-CCP fusion protein in which the CCP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant CCP.

In another embodiment, the fusion protein is a CCP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., plant or mammalian host cells), expression and/or secretion of CCP can be increased through use of a heterologous signal sequence.

The CCP fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a plant or a subject *in vivo*. The CCP fusion proteins can be used to affect the bioavailability of a CCP substrate. Use of CCP fusion proteins may be useful agriculturally for the increase of crop yields or therapeutically for the treatment of cellular growth related disorders, e.g., cancer. Moreover, the CCP-fusion proteins of the invention can be used as immunogens to produce anti-CCP antibodies in a subject, to purify CCP ligands and in screening assays to identify molecules which inhibit the interaction of CCP with a CCP substrate, e.g., a kinase such as CDC2b.

Preferably, a CCP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A CCP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the CCP protein.

The present invention also pertains to variants of the CCP proteins which function as either CCP agonists (mimetics) or as CCP antagonists. Variants of the CCP proteins can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of a CCP protein. An agonist of the CCP proteins can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of a CCP protein. An antagonist of a CCP protein can inhibit one or more of the activities of the naturally occurring form of the CCP protein by, for example, competitively modulating a cellular activity of a CCP protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the CCP protein.

In one embodiment, variants of a CCP protein which function as either CCP agonists (mimetics) or as CCP antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of a CCP protein for CCP protein agonist or antagonist activity. In one embodiment, a variegated library of CCP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of CCP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential CCP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of CCP sequences therein. There are a variety of methods which can be used to produce libraries of potential CCP variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential CCP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of a CCP protein coding sequence can be used to generate a variegated population of CCP fragments for screening and subsequent selection of variants of a CCP protein. In one embodiment, a library of coding sequence fragments

can be generated by treating a double stranded PCR fragment of a CCP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single
5 stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the CCP protein.

Several techniques are known in the art for screening gene products of
10 combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of CCP proteins. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into
15 replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the
20 screening assays to identify CCP variants (Arkin and Yourvan (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In one embodiment, cell based assays can be exploited to analyze a variegated CCP library. For example, a library of expression vectors can be transfected into a cell line which ordinarily synthesizes and secretes CCP. The transfected cells are then cultured
25 such that CCP and a particular mutant CCP are secreted and the effect of expression of the mutant on CCP activity in cell supernatants can be detected, *e.g.*, by any of a number of enzymatic assays. Plasmid DNA can then be recovered from the cells which score for inhibition, or alternatively, potentiation of CCP activity, and the individual clones further characterized.

30 An isolated CCP protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind CCP using standard techniques for polyclonal and monoclonal antibody preparation. A full-length CCP protein can be used or, alternatively, the invention provides antigenic peptide fragments of CCP for use as immunogens. The antigenic peptide of CCP comprises at least 8 amino acid residues and
35 encompasses an epitope of CCP such that an antibody raised against the peptide forms a specific immune complex with CCP. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more

preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues.

Preferred epitopes encompassed by the antigenic peptide are regions of CCP that are located on the surface of the protein, *e.g.*, hydrophilic regions.

5 A CCP immunogen typically is used to prepare antibodies by immunizing a suitable subject, (*e.g.*, rabbit, goat, mouse or other mammal) with the immunogen. An appropriate immunogenic preparation can contain, for example, recombinantly expressed CCP protein or a chemically synthesized CCP polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or similar
10 immunostimulatory agent. Immunization of a suitable subject with an immunogenic CCP preparation induces a polyclonal anti-CCP antibody response.

Accordingly, another aspect of the invention pertains to anti-CCP antibodies. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen
15 binding site which specifically binds (immunoreacts with) an antigen, such as CCP. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind CCP. The term "monoclonal antibody" or "monoclonal antibody composition", as used
20 herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of CCP. A monoclonal antibody composition thus typically displays a single binding affinity for a particular CCP protein with which it immunoreacts.

Polyclonal anti-CCP antibodies can be prepared as described above by immunizing
25 a suitable subject with a CCP immunogen. The anti-CCP antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized CCP. If desired, the antibody molecules directed against CCP can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography to
30 obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the anti-CCP antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497) (see also, Brown *et al.* (1981) *J. Immunol.* 127:539-46; Brown *et al.* (1980) *J. Biol. Chem.* 255:4980-83; Yeh *et al.* (1976) *Proc. Natl. Acad. Sci. USA* 76:2927-31; and Yeh *et al.* (1982) *Int. J. Cancer* 29:269-75), the more recent human B cell hybridoma technique (Kozbor *et al.* (1983) *Immunol Today* 4:72), the EBV-hybridoma technique (Cole *et al.* (1985), *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or
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trionoma techniques. The technology for producing monoclonal antibody hybridomas is well known (see generally R. H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); E. A. Lerner (1981) *Yale J. Biol. Med.*, 54:387-402; M. L. Gefter *et al.* (1977) *Somatic Cell Genet.* 3:231-36). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with a CCP immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds CCP.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating an anti-CCP monoclonal antibody (see, *e.g.*, G. Galfre *et al.* (1977) *Nature* 266:55052; Gefter *et al.* *Somatic Cell Genet.*, cited *supra*; Lerner, *Yale J. Biol. Med.*, cited *supra*; Kenneth, *Monoclonal Antibodies*, cited *supra*). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods which also would be useful. Typically, the immortal cell line (*e.g.*, a myeloma cell line) is derived from the same mammalian species as the lymphocytes. For example, murine hybridomas can be made by fusing lymphocytes from a mouse immunized with an immunogenic preparation of the present invention with an immortalized mouse cell line. Preferred immortal cell lines are mouse myeloma cell lines that are sensitive to culture medium containing hypoxanthine, aminopterin and thymidine ("HAT medium"). Any of a number of myeloma cell lines can be used as a fusion partner according to standard techniques, *e.g.*, the P3-NS1/1-Ag4-1, P3-x63-Ag8.653 or Sp2/O-Ag14 myeloma lines. These myeloma lines are available from ATCC. Typically, HAT-sensitive mouse myeloma cells are fused to mouse splenocytes using polyethylene glycol ("PEG"). Hybridoma cells resulting from the fusion are then selected using HAT medium, which kills unfused and unproductively fused myeloma cells (unfused splenocytes die after several days because they are not transformed). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind CCP, *e.g.*, using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal anti-CCP antibody can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with CCP to thereby isolate immunoglobulin library members that bind CCP. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™ Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, Ladner *et al.* U.S. Patent No. 5,223,409; Kang *et al.* PCT

International Publication No. WO 92/18619; Dower *et al.* PCT International Publication No. WO 91/17271; Winter *et al.* PCT International Publication WO 92/20791; Markland *et al.* PCT International Publication No. WO 92/15679; Breitling *et al.* PCT International Publication WO 93/01288; McCafferty *et al.* PCT International Publication No. WO 92/01047; Garrard *et al.* PCT International Publication No. WO 92/09690; Ladner *et al.* PCT International Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275-1281; Griffiths *et al.* (1993) *EMBO J* 12:725-734; Hawkins *et al.* (1992) *J. Mol. Biol.* 226:889-896; Clarkson *et al.* (1991) *Nature* 352:624-628; Gram *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:3576-3580; Garrad *et al.* (1991) *Bio/Technology* 9:1373-1377; Hoogenboom *et al.* (1991) *Nuc. Acid Res.* 19:4133-4137; Barbas *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88:7978-7982; and McCafferty *et al.* *Nature* (1990) 348:552-554.

Additionally, recombinant anti-CCP antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in Robinson *et al.* International Application No. PCT/US86/02269; Akira, *et al.* European Patent Application 184,187; Taniguchi, M., European Patent Application 171,496; Morrison *et al.* European Patent Application 173,494; Neuberger *et al.* PCT International Publication No. WO 86/01533; Cabilly *et al.* U.S. Patent No. 4,816,567; Cabilly *et al.* European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J. Immunol.* 139:3521-3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Canc. Res.* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559; Morrison, S. L. (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; Winter U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

An anti-CCP antibody (*e.g.*, monoclonal antibody) can be used to isolate CCP by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-CCP antibody can facilitate the purification of natural CCP from cells and of recombinantly produced CCP expressed in host cells. Moreover, an anti-CCP antibody can be used to detect CCP protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the CCP protein. These antibodies can also be used, for example, for the immunoprecipitation and immunolocalization of proteins according to the invention as well as for the monitoring of the synthesis of such proteins,

for example, in recombinant organisms, and for the identification of compounds interacting with the protein according to the invention.

Anti-CCP antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

III. Computer Readable Means

The CCP nucleotide sequences of the invention (*e.g.*, SEQ ID NO:1-66 or 228-239) or amino acid sequences of the invention (*e.g.*, SEQ ID NO:67-132, 205, 211, 215-216, or 220-227) are also provided in a variety of mediums to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid or amino acid molecule, which contains a nucleotide or amino acid sequences of the present invention. Such a manufacture provides the nucleotide or amino acid sequences, or a subset thereof (*e.g.*, a subset of open reading frames (ORI's)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the nucleotide or amino acid sequences, or a subset thereof, as they exist in nature or in purified form.

In one application of this embodiment, a nucleotide or amino acid sequence of the present invention can be recorded on computer readable media. As used herein "computer readable media" includes any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. The skilled artisan will readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide or amino acid sequence of the present invention.

As used herein "recorded" refers to a process of storing information on computer readable medium. The skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising the nucleotide or amino acid sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide or amino acid sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase Oracle, or the like. The skilled artisan can readily adapt any number of dataprocessor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide or amino acid sequences of the invention in computer readable form, the skilled artisan can routinely access the sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the invention in computer readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identity fragments or regions of the sequences of the invention which match a particular target sequence or target motif.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotide or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium for analysis and comparison to other sequences. A variety of known algorithms are disclosed publicly and a variety of commercially available software of conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPatter (EMBL), BLASTN and BASTX (NCBIA).

For example, software which implements the BLAST (Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410) and BLAZE (Brutlag *et al.* (1993) *Comp. Chem.* 17:203-207) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) of the sequences of the invention which contain homology to ORFs or proteins from other libraries. Such ORFs are protein encoding fragments and are useful in producing commercially important proteins such as enzyme used in various reactions and in the production of commercially useful metabolites.

IV. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a CCP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, *e.g.*, a plant cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant

expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, CCP proteins, mutant forms of CCP proteins, fusion proteins, and the like).

The vectors of the invention comprise a selectable and/or scorable marker. Selectable marker genes useful for the selection of transformed plant cells, callus, plant tissue and plants are well known to those skilled in the art and comprise, for example, antimetabolite resistance as the basis of selection for dhfr, which confers resistance to methotrexate (Reiss, *Plant Physiol. (Life Sci. Adv.)* 13 (1994), 143-149); npt, which confers resistance to the aminoglycosides neomycin, kanamycin and paromycin (Herrera-Estrella, *EMBO J.* 2 (1983), 987-995) and hyg, which confers resistance to hygromycin (Marsh, *Gene* 32 (1984), 481-485). Additional selectable genes have been described, namely trpB, which allow cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histidinol in place of histidine (Hartman, *Proc. Natl. Acad. Sci. USA* 85 (1988), 8047); mannose-6-phosphate isomerase which allows cells to utilize mannose (WO 94/20627) and ODC (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO (McConlogue, 1987, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.) or deaminase from *Aspergillus terreus* which confers resistance to Blasticidin S (Tamura, *Biosci. Biotechnol. Biochem.* 59 (1995), 2336-2338).

Useful scorable markers are also known to those skilled in the art and are commercially available. Advantageously, the marker is a gene encoding luciferase (Giacomin, *Pl. Sci.* 116 (1996), 59-72; Scikantha, *J. Bact.* 178 (1996), 121), green fluorescent protein (Gerdes, *FEBS Lett.* 389 (1996), 44-47) or β -glucuronidase (Jefferson, *EMBO J.* 6 (1987), 3901-3907). This embodiment is particularly useful for simple and rapid screening of cells, tissues and organisms containing a vector of the invention.

A "plant promoter" is a promoter capable of initiating transcription in plant cells. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria. Preferred promoters may contain additional copies of one or more specific regulatory elements, to further enhance expression and/or to alter the spatial expression and/or temporal expression of a nucleic acid molecule to which it is operably connected. For example, copper-responsive, glucocorticoid-responsive or dexamethasone-responsive regulatory elements may be placed adjacent to a heterologous promoter sequence driving expression of a nucleic acid molecule to confer copper inducible, glucocorticoid-inducible, or dexamethasone-inducible expression respectively, on said nucleic acid molecule. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, seeds, endosperm, embryos, fibers, xylem vessels, tracheids, or sclerenchyma. Such promoters are referred to as "tissue preferred." Promoters which initiate transcription only in certain tissue are referred to as "tissue specific." A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter which is active under most environmental conditions.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a CCP protein can be expressed in plant cells, bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or

transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

Means for introducing a recombinant expression vector of this invention into plant tissue or cells include, but are not limited to; transformation using CaCl_2 and variations thereof, in particular the method described by Hanahan (J. Mol.Biol. 166, 557-560, 1983), direct DNA uptake into protoplasts (Krens *et al.*, Nature 296: 72-74, 1982; Paszkowski *et al.*, EMBO J. 3:2717-2722, 1984), PEG-mediated uptake to protoplasts (Armstrong *et al.*, Plant Cell Reports 9: 335-339, 1990) microparticle bombardment, electroporation (Fromm *et al.*, Proc. Natl. Acad. Sci. (USA) 82:5824-5828, 1985), microinjection of DNA (Crossway *et al.*, Mol. Gen. Genet. 202:179-185, 1986), microparticle bombardment of tissue explants or cells (Christou *et al.*, Plant Physiol 87: 671-674, 1988; Sanford, Particulate Science and Technology 5: 27-37, 1987), vacuum-infiltration of tissue with nucleic acid, or in the case of plants, T-DNA-mediated transfer from *Agrobacterium* to the plant tissue as described essentially by An *et al.* (EMBO J 4:277-284, 1985), Herrera-Estrella *et al.* (Nature 303: 209-213, 1983a; EMBO J. 2: 987-995, 1983b; In: Plant Genetic Engineering, Cambridge University Press, N.Y., pp 63-93, 1985), or *in planta* method using *Agrobacterium tumefaciens* such as that described by Bechtold *et al.*, (C.R. Acad. Sci. (Paris, Sciences de la vie/ Life Sciences) 316: 1194-1199, 1993), Clough *et al.* (Plant J. 16: 735-743, 1998), Trieu *et al.* (Plant J. 22:531-541, 2000) or Kloti (WO01/12828, 2001). Methods for transformation of monocotyledonous plants are well known in the art and include *Agrobacterium*-mediated transformation (Cheng *et al.* (1997) WO 97/48814; Hansen (1998) WO 98/54961; Hiei *et al.* (1994) WO 94/00977; Hiei *et al.* (1998) WO 98/17813; Rikiishi *et al.* (1999) WO 99/04618; Saito *et al.* (1995) WO 95/06722), microprojectile bombardment (Adams *et al.* (1999) US 5,969,213; Bowen *et al.* (1998) US 5,736,369; Chang *et al.* (1994) WO 94/13822; Lundquist *et al.* (1999) US 5,874,265/US 5,990,390; Vasil and Vasil (1995) US 5,405,765; Walker *et al.* (1999) US 5,955,362), DNA uptake (Eval *et al.* (1993) WO 93/181,168), microinjection of *Agrobacterium* cells (von Holt 1994 DE 4309203), sonication (Finer *et al.* (1997) US 5,693,512) and flower-dip or *in planta*- transformation (Kloti, WO01/12828, 2001).

The vector DNA may further comprise a selectable marker gene to facilitate the identification and/or selection of cells which are transfected or transformed with a genetic construct. Suitable selectable marker genes contemplated herein include the ampicillin resistance (Amp^r), tetracycline resistance gene (Tc^r), bacterial kanamycin resistance gene (Kan^r), phosphinothricin resistance gene, neomycin phosphotransferase gene (*nptII*), hygromycin resistance gene, β -glucuronidase (GUS) gene, chloramphenicol acetyltransferase (CAT) gene, green fluorescent protein (*gfp*) gene (Haseloff *et al.*, 1997), and luciferase gene.

For microparticle bombardment of cells, a microparticle is propelled into a cell to produce a transformed cell. Any suitable ballistic cell transformation methodology and apparatus can be used in performing the present invention. Exemplary apparatus and procedures are disclosed by Stomp *et al.* (U.S. Patent No. 5,122,466) and Sanford and Wolf (U.S. Patent No. 4,945,050). When using ballistic transformation procedures, the gene construct may incorporate a plasmid capable of replicating in the cell to be transformed. Examples of microparticles suitable for use in such systems include 1 to 5 μm gold spheres. The DNA construct may be deposited on the microparticle by any suitable technique, such as by precipitation.

A whole plant may be regenerated from the transformed or transfected cell, in accordance with procedures well known in the art. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a gene construct of the present invention and a whole plant regenerated therefrom. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (*e.g.*, apical meristem, axillary buds, and root meristems), and induced meristem tissue (*e.g.*, cotyledon meristem and hypocotyl meristem).

The term "organogenesis", as used herein, includes a process by which shoots and roots are developed sequentially from meristematic centres.

The term "embryogenesis", as used herein, includes a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes.

Preferably, the plant is produced according to the methods of the invention by transfecting or transforming the plant with a genetic sequence, or by introducing to the plant a protein, by any art-recognized means, such as microprojectile bombardment, microinjection, *Agrobacterium*-mediated transformation (including *in planta* transformation), protoplast fusion, or electroporation, amongst others. Most preferably the plant is produced by *Agrobacterium*-mediated transformation.

Agrobacterium-mediated transformation or agrolistic transformation of plants, yeast, moulds or filamentous fungi is based on the transfer of part of the transformation vector sequences, called the T-DNA, to the nucleus and on integration of said T-DNA in the genome of said eukaryote.

The term "*Agrobacterium*" as used herein, includes a member of the *Agrobacteriaceae*, more preferably *Agrobacterium* or *Rhizobacterium* and most preferably *Agrobacterium tumefaciens*.

The term "T-DNA", or "transferred DNA", as used herein, includes the transformation vector flanked by T-DNA borders which is, after activation of the *Agrobacterium vir* genes, nicked at the T-DNA borders and is transferred as a single stranded DNA to the nucleus of an eukaryotic cell.

5 As used herein, the terms "T-DNA borders", "T-DNA border region", or "border region" include either right T-DNA borders (RB) or left T-DNA borders (LB), which comprise a core sequence flanked by a border inner region as part of the T-DNA flanking the border and/or a border outer region as part of the vector backbone flanking the border. The core sequences comprise 22 bp in case of octopine-type vectors and 25 bp in case of
10 nopaline-type vectors. The core sequences in the right border region and left border region form imperfect repeats.

As used herein, the term "T-DNA transformation vector" or "T-DNA vector" includes any vector encompassing a T-DNA sequence flanked by a right and left T-DNA border consisting of at least the right and left border core sequences, respectively, and used
15 for transformation of any eukaryotic cell.

As used herein, the term "T-DNA vector backbone sequence" or "T-DNA vector backbone sequences" includes all DNA of a T-DNA containing vector that lies outside of the T-DNA borders and, more specifically, outside the nicking sites of the border core imperfect repeats.

20 The present invention includes optimized T-DNA vectors such that vector backbone integration in the genome of a eukaryotic cell is minimized or absent. The term "optimized T-DNA vector" as used herein includes a T-DNA vector designed either to decrease or abolish transfer of vector backbone sequences to the genome of a eukaryotic cell. Such T-DNA vectors are known to the one of skill in the art and include those
25 described by Hanson *et al.* (1999) and by Stuiver *et al.* (1999 - WO9901563).

The current invention clearly considers the inclusion of a DNA sequence encoding a CCP, homologue, analogue, derivative or immunologically active fragment thereof as defined supra, in any T-DNA vector comprising binary transformation vectors, super-binary transformation vectors, co-integrate transformation vectors, Ri-derived
30 transformation vectors as well as in T-DNA carrying vectors used in agroclistic transformation.

As used herein, the term "binary transformation vector" includes a T-DNA transformation vector comprising: a T-DNA region comprising at least one gene of interest and/or at least one selectable marker active in the eukaryotic cell to be transformed; and
35 a vector backbone region comprising at least origins of replication active in *E. coli* and *Agrobacterium* and markers for selection in *E. coli* and *Agrobacterium*. Alternatively, replication of the binary transformation vector in *Agrobacterium* is dependent on the presence of a separate helper plasmid. The binary vector pGreen and the helper plasmid

pSoup form an example of such a system (Hellens et al. (2000), Plant Mol. Biol. 42, 819-832; <http://www.pgreen.ac.uk>).

The T-DNA borders of a binary transformation vector can be derived from octopine-type or nopaline-type Ti plasmids or from both. The T-DNA of a binary vector is only transferred to a eukaryotic cell in conjunction with a helper plasmid. As used herein, the term "helper plasmid" includes a plasmid that is stably maintained in *Agrobacterium* and is at least carrying the set of *vir* genes necessary for enabling transfer of the T-DNA. The set of *vir* genes can be derived from either octopine-type or nopaline-type Ti plasmids or from both.

As used herein, the term "super-binary transformation vector" includes a binary transformation vector additionally carrying in the vector backbone region a *vir* region of the Ti plasmid pTiBo542 of the super-virulent *A. tumefaciens* strain A281 (EP0604662, EP0687730). Super-binary transformation vectors are used in conjunction with a helper plasmid.

As used herein, the term "co-integrate transformation vector" includes a T-DNA vector at least comprising: a T-DNA region comprising at least one gene of interest and/or at least one selectable marker active in plants; and a vector backbone region comprising at least origins of replication active in *Escherichia coli* and *Agrobacterium*, and markers for selection in *E. coli* and *Agrobacterium*, and a set of *vir* genes necessary for enabling transfer of the T-DNA. The T-DNA borders and the set of *vir* genes of the T-DNA vector can be derived from either octopine-type or nopaline-type Ti plasmids or from both.

The term "Ri-derived plant transformation vector" includes a binary transformation vector in which the T-DNA borders are derived from a Ti plasmid and the binary transformation vector being used in conjunction with a 'helper' Ri-plasmid carrying the necessary set of *vir* genes.

The terms "agrolistics", "agrolistic transformation" or "agrolistic transfer" include a transformation method combining features of *Agrobacterium*-mediated transformation and of biolistic DNA delivery. As such, a T-DNA containing target plasmid is co-delivered with DNA/RNA enabling in planta production of VirD1 and VirD2 with or without VirE2 (Hansen and Chilton 1996; Hansen et al. 1997; Hansen and Chilton 1997 - WO9712046).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a CCP protein. Accordingly, the invention further provides methods for producing a CCP protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a CCP protein has been introduced) in a suitable medium such that a CCP protein is produced. In another embodiment, the method further comprises isolating a CCP protein from the medium or the host cell.

The host cells of the invention can also be used to produce transgenic plant or non-human transgenic animals in which exogenous CCP sequences have been introduced into their genome or homologous recombinant plants or animals in which endogenous CCP sequences have been altered. Such plants and animals are useful for studying the function and/or activity of a CCP and for identifying and/or evaluating modulators of CCP activity.

Trangenic Plants

As used herein, "transgenic plant" includes a plant which comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well as those created by sexual crosses as asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring event such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

A transgenic plant of the invention can be created by introducing a CCP-encoding nucleic acid into the plant by placing it under the control of regulatory elements which ensure the expression in plant cells. These regulatory elements may be heterologous or homologous with respect to the nucleic acid molecule to be expressed as well with respect to the plant species to be transformed. In general, such regulatory elements comprise a promoter active in plant cells. These promoters can be used to modulate (*e.g.* increase or decrease) CCP content and/or composition in a desired tissue. To obtain expression in all tissues of a transgenic plant, preferably constitutive promoters are used, such as the 35 S promoter of CaMV (Odell, *Nature* 313 (1985), 810-812) or promoters from such genes as rice actin (McElroy *et al.* (1990) *Plant Cell* 2:163-171) maize H3 histone (Lepetit *et al.* (1992) *Mol. Gen. Genet* 231:276-285) or promoters of the polyubiquitin genes of maize (Christensen, *Plant Mol. Biol.* 18 (1982), 675-689). In order to achieve expression in specific tissues of a transgenic plant it is possible to use tissue specific promoters (see, *e.g.*, Stockhaus, *EMBO J.* 8 (1989), 2245-2251 or Table II, below).

Table II:

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
α -amylase (<i>Amy32b</i>)	aleurone	Lanahan, M.B., <i>et al.</i> , <i>Plant Cell</i> 4:203-211, 1992; Skriver, K., <i>et al.</i> <i>Proc. Natl. Acad. Sci. (USA)</i> 88: 7266-7270, 1991
cathepsin β -like gene	aleurone	Cejudo, F.J., <i>et al.</i> <i>Plant Molecular Biology</i> 20:849-856, 1992.
<i>Agrobacterium rhizogenes rolB</i>	cambium	Nilsson <i>et al.</i> , <i>Physiol. Plant.</i> 100:456-462, 1997
PRP genes	cell wall	http://salus.medium.edu/mmg/tierney/html
barley <i>lir1</i> promoter	endosperm	
synthetic promoter	endosperm	Vicente-Carbajosa <i>et al.</i> , <i>Plant J.</i> 13: 629-640, 1998.
AtPRP4	flowers	http://salus.medium.edu/mmg/tierney/html
chalcone synthase (<i>chsA</i>)	flowers	Van der Meer, <i>et al.</i> , <i>Plant Mol. Biol.</i> 15, 95-109, 1990.
LAT52	anther	Twiss <i>et al.</i> <i>Mol. Gen. Genet.</i> 217:240-245 (1989)
<i>apetala-3</i>	flowers	
chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; http://winetitles.com.au/gwrdc/csh95-1.html
<i>rbcs-3A</i>	green tissue (eg leaf)	Lam, E. <i>et al.</i> , <i>The Plant Cell</i> 2: 857-866, 1990.; Tucker <i>et al.</i> , <i>Plant Physiol.</i> 113: 1303-1308, 1992.
leaf-specific genes	leaf	Baszczynski, <i>et al.</i> , <i>Nucl. Acid Res.</i> 16: 4732, 1988.
AtPRP4	leaf	http://salus.medium.edu/mmg/tierney/html
<i>Pinus cab-6</i>	leaf	Yamamoto <i>et al.</i> , <i>Plant Cell Physiol.</i> 35:773-778, 1994.
SAM22	senescent leaf	Crowell, <i>et al.</i> , <i>Plant Mol. Biol.</i> 18: 459-466, 1992.
<i>R. japonicum nif</i> gene	nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	nodule	United States Patent No. 5, 008, 194
GmENOD40	nodule	Yang, <i>et al.</i> , <i>The Plant J.</i> 3: 573-585.
PEP carboxylase (PEPC)	nodule	Pathirana, <i>et al.</i> , <i>Plant Mol. Biol.</i> 20: 437-450, 1992.
leghaemoglobin (Lb)	nodule	Gordon, <i>et al.</i> , <i>J. Exp. Bot.</i> 44: 1453-1465, 1993.
<i>Tungro bacilliform virus</i> gene	phloem	Bhattacharyya-Pakrasi, <i>et al.</i> , <i>The Plant J.</i> 4: 71-79, 1992.
sucrose-binding protein gene	plasma membrane	Grimes, <i>et al.</i> , <i>The Plant Cell</i> 4:1561-1574, 1992.

pollen-specific genes	pollen; microspore	Albani, <i>et al.</i> , <i>Plant Mol. Biol.</i> 15: 605, 1990; Albani, <i>et al.</i> , <i>Plant Mol. Biol.</i> 16: 501, 1991)
Zm13	pollen	Guerrero <i>et al</i> <i>Mol. Gen. Genet.</i> 224:161-168 (1993)
apg gene	microspore	Twell <i>et al</i> <i>Sex. Plant Reprod.</i> 6:217-224 (1993)
maize pollen-specific gene	pollen	Hamilton, <i>et al.</i> , <i>Plant Mol. Biol.</i> 18: 211-218, 1992.
sunflower pollen-expressed gene	pollen	Baltz, <i>et al.</i> , <i>The Plant J.</i> 2: 713-721, 1992.
<i>B. napus</i> pollen-specific gene	pollen;anther; tapetum	Arnoldo, <i>et al.</i> , <i>J. Cell. Biochem.</i> , Abstract No. Y101, 204, 1992.
root-expressible genes	roots	Tingey, <i>et al.</i> , <i>EMBO J.</i> 6: 1, 1987.
tobacco auxin-inducible gene	root tip	Van der Zaal, <i>et al.</i> , <i>Plant Mol. Biol.</i> 16, 983, 1991.
β -tubulin	root	Oppenheimer, <i>et al.</i> , <i>Gene</i> 63: 87, 1988.
tobacco root-specific genes	root	Conkling, <i>et al.</i> , <i>Plant Physiol.</i> 93: 1203, 1990.
<i>B. napus</i> G1-3b gene	root	United States Patent No. 5, 401, 836
SbPRP1	roots	Suzuki <i>et al.</i> , <i>Plant Mol. Biol.</i> 21: 109-119, 1993.
AtPRP1; AtPRP3	roots; root hairs	http://salus.medium.edu/mmg/tierney/html
RD2 gene	root cortex	http://www2.cnsu.edu/ncsu/research
TobRB7 gene	root vasculature	http://www2.cnsu.edu/ncsu/research
AtPRP4	leaves; flowers; lateral root primordia	http://salus.medium.edu/mmg/tierney/html
seed-specific genes	seed	Simon, <i>et al.</i> , <i>Plant Mol. Biol.</i> 5: 191, 1985; Scofield, <i>et al.</i> , <i>J. Biol. Chem.</i> 262: 12202, 1987.; Baszczynski, <i>et al.</i> , <i>Plant Mol. Biol.</i> 14: 633, 1990.
Brazil Nut albumin	seed	Pearson, <i>et al.</i> , <i>Plant Mol. Biol.</i> 18: 235-245, 1992.
legumin	seed	Ellis, <i>et al.</i> , <i>Plant Mol. Biol.</i> 10: 203-214, 1988.
glutelin (rice)	seed	Takaiwa, <i>et al.</i> , <i>Mol. Gen. Genet.</i> 208: 15-22, 1986; Takaiwa, <i>et al.</i> , <i>FEBS Letts.</i> 221: 43-47, 1987.
zein	seed	Matzke <i>et al</i> <i>Plant Mol Biol</i> , 14(3):323-32 1990

napA	seed	Stalberg, <i>et al</i> , <i>Planta</i> 199: 515-519, 1996.
sunflower oleosin	seed (embryo and dry seed)	Cummins, <i>et al</i> , <i>Plant Mol. Biol.</i> 19: 873-876, 1992
<i>LEAFY</i>	shoot meristem	Weigel <i>et al</i> , <i>Cell</i> 69:843-859, 1992.
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
<i>CLAVATA1</i>	shoot meristem	Accession number AF049870
stigma-specific genes	stigma	Nasrallah, <i>et al</i> , <i>Proc. Natl. Acad. Sci. USA</i> 85: 5551, 1988; Trick, <i>et al</i> , <i>Plant Mol. Biol.</i> 15: 203, 1990.
class I patatin gene	tuber	Liu <i>et al</i> , <i>Plant Mol. Biol.</i> 153:386-395, 1991.
<i>blz2</i>	endosperm	EP99106056.7
PCNA rice	meristem	Kosugi <i>et al</i> , <i>Nucleic Acids Research</i> 19:1571-1576, 1991; Kosugi S. and Ohashi Y, <i>Plant Cell</i> 9:1607-1619, 1997.

The promoters listed in the foregoing table are provided for the purposes of exemplification only and the present invention is not to be limited by the list provided therein. Those skilled in the art will readily be in a position to provide additional promoters that are useful in performing the present invention. The promoters listed may also be modified to provide specificity of expression as required.

Known are also promoters which are specifically active in tubers of potatoes or in seeds of different plants species, such as maize, Vicia, wheat, barley and the like. Inducible promoters may be used in order to be able to exactly control expression under certain environmental or developmental conditions such as pathogens, anaerobia, or light. Examples of inducible promoters include the promoters of genes encoding heat shock proteins or microspore-specific regulatory elements (WO96/16182). Furthermore, the chemically inducible Tet-system may be employed (Gatz, *Mol. Gen. Genet.* 227 (1991); 229-237). Further suitable promoters are known to the person skilled in the art and are described, e.g., in Ward (*Plant Mol. Biol.* 22 (1993), 361-366). The regulatory elements may further comprise transcriptional and/or translational enhancers functional in plants cells. Furthermore, the regulatory elements may include transcription termination signals, such as a poly-A signal, which lead to the addition of a poly A tail to the transcript which may improve its stability.

In the case that a nucleic acid molecule according to the invention is expressed in the sense orientation, the coding sequence can be modified such that the protein is located in any desired compartment of the plant cell, *e.g.*, the nucleus, endoplasmatic reticulum, the vacuole, the mitochondria, the plastids, the apoplast, or the cytoplasm.

5 Methods for the introduction of foreign DNA into plants are also well known in the art. These include, for example, the transformation of plant cells or tissues with T-DNA using *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*, the fusion of protoplasts, direct gene transfer (see, *e.g.*, EP-A 164 575), injection, electroporation, biolistic methods like particle bombardment, pollen-mediated transformation, plant RNA virus-mediated
10 transformation, liposome-mediated transformation, transformation using wounded or enzyme-degraded immature embryos, or wounded or enzyme-degraded embryogenic callus and other methods known in the art. The vectors used in the method of the invention may contain further functional elements, for example "left border"- and "right border"-sequences of the T-DNA of *Agrobacterium* which allow for stably integration into the
15 plant genome. Furthermore, methods and vectors are known to the person skilled in the art which permit the generation of marker free transgenic plants, *i.e.*, the selectable or scorable marker gene is lost at a certain stage of plant development or plant breeding. This can be achieved by, for example, cotransformation (Lyznik, *Plant Mol. Biol.* 13 (1989), 151-161; Peng, *Plant Mol. Biol.* 27 (1995), 91-104) and/or by using systems which utilize enzymes
20 capable of promoting homologous recombination in plants (see, *e.g.*, WO97/08331; Bayley, *Plant Mol. Biol.* 18 (1992), 353-361; Lloyd, *Mol. Gen. Genet.* 242 (1994), 653-657; Maeser, *Mol. Gen. Genet.* 230 (1991), 170-176; Onouchi, *Nucl. Acids Res.* 19 (1991), 6373-6378). Methods for the preparation of appropriate vectors are described by, *e.g.*, Sambrook (*Molecular Cloning; A Laboratory Manual*, 2nd Edition (1989), Cold
25 Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

Suitable strains of *Agrobacterium tumefaciens* and vectors, as well as transformation of *Agrobacteria*, and appropriate growth and selection media are described in, for example, GV3101 (pMK90RK), Koncz, *Mol. Gen. Genet.* 204 (1986), 383-396; C58C1 (pGV 3850kan), Deblaere, *Nucl. Acid Res.* 13 (1985), 4777; Bevan, *Nucleic. Acid*
30 *Res.* 12(1984), 8711; Koncz, *Proc. Natl. Acad. Sci. USA* 86 (1989), 8467-8471; Koncz, *Plant Mol. Biol.* 20 (1992), 963-976; Koncz, *Specialized vectors for gene tagging and expression studies*. In: *Plant Molecular Biology Manual Vol 2*, Gelvin and Schilperoort (Eds.), Dordrecht, The Netherlands: Kluwer Academic Publ. (1994), 1-22; EP-A-120 516; Hoekema: *The Binary Plant Vector System*, Offsetdrukkerij Kanters B.V., Alblasserdam
35 (1985), Chapter V, Fraley, *Crit. Rev. Plant. Sci.*, 4, 1-46; An, *EMBO J.* 4 (1985), 277-287). Although the use of *Agrobacterium tumefaciens* is preferred in the method of the invention, other *Agrobacterium* strains, such as *Agrobacterium rhizogenes*, may be used, for example, if a phenotype conferred by said strain is desired.

Methods for the transformation using biolistic methods are known to the person skilled in the art; see, *e.g.*, Wan, *Plant Physiol.* 104 (1994), 37-48; Vasil, *Bio/Technology* 11 (1993), 1553-1558 and Christou (1996) *Trends in Plant Science* 1, 423-431. Microinjection can be performed as described in Potrykus and Spangenberg (eds.), *Gene Transfer To Plants*.
5 Springer Verlag, Berlin, NY (1995).

The transformation of most dicotyledonous plants may be performed using the methods described above or using transformation via biolistic methods as, *e.g.*, described above as well as protoplast transformation, electroporation of partially permeabilized cells, or introduction of DNA using glass fibers.

10 In general, the plants which are modified according to the invention may be derived from any desired plant species. They can be monocotyledonous plants or dicotyledonous plants, preferably they belong to plant species of interest in agriculture, wood culture or horticulture interest, such as crop plants (*e.g.*, maize, rice, barley, wheat, rye, oats), potatoes, oil producing plants (*e.g.*, oilseed rape, sunflower, pea nut, soy bean), cotton, sugar beet,
15 sugar cane, leguminous plants (*e.g.*, beans, peas), or wood producing plants, preferably trees.

The present invention also relates to a transgenic plant cell which contains (preferably stably integrated into its genome) a nucleic acid molecule of the present invention linked to regulatory elements which allow expression of the nucleic acid molecule in plant cells. The presence and expression of the nucleic acid molecule in the transgenic plant cells leads to the
20 synthesis of a CCP protein and may lead to physiological and phenotypic changes in plants containing such cells.

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype. Such regeneration techniques often rely on manipulation of certain
25 phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced with a polynucleotide of the present invention.

Plant cells transformed with a plant expression vector can be regenerated, *e.g.*, from single cells, callus tissue or leaf discs according to standard plant tissue culture techniques.
30 It is well known in the art that various cells, tissues, and organs from almost any plant can be successfully cultured to regenerate an entire plant. Plant regeneration from cultured protoplasts is described in Evans *et al.*, *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, Macmillan Publishing Company, New York, pp. 124-176 (1983); and *Binding, Regeneration of Plants, Plant Protoplasts*, CRC Press, Boca Raton, pp. 21-73
35 (1985).

Transformed plant cells, calli or explant can be cultured on regeneration medium in the dark for several weeks, generally about 1 to 3 weeks to allow the somatic embryos to mature. Preferred regeneration media include media containing MS salts, such as PHI-E

and PHI-F media. The plant cells, calli or explant are then typically cultured on rooting medium in a light/dark cycle until shoots and roots develop. Methods for plant regeneration are known in the art and preferred methods are provided by Kamo *et al.*, (*Bot. Gaz.* 146(3):324-334, 1985), West *et al.*, (*The Plant Cell* 5:1361-1369, 1993), and Duncan *et al.* (*Planta* 165:322-332, 1985).

Small plantlets can then be transferred to tubes containing rooting medium and allowed to grow and develop more roots for approximately another week. The plants can then be transplanted to soil mixture in pots in the greenhouse.

The regeneration of plants containing the foreign gene introduced by *Agrobacterium* from leaf explants can be achieved as described by Horsch *et al.*, *Science*, 227:1229-1231 (1985). In this procedure, transformants are grown in the presence of a selection agent and in a medium that induces the regeneration of shoots in the plant species being transformed as described by Fraley *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 80:4803 (1983). This procedure typically produces shoots within two to four weeks and these transformant shoots are then transferred to an appropriate root-inducing medium containing the selective agent and an antibiotic to prevent bacterial growth. Transgenic plants of the present invention may be fertile or sterile.

Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee *et al.*, *Ann. Rev. of Plant Phys.*, 38:467-486(1987). The regeneration of plants from either single plant protoplasts or various explants is well known in the art. See, for example, *Methods for Plant Molecular Biology*, A. Weissbach and H. Weissbach, eds., Academic Press, Inc., San Diego, Calif. (1988). This regeneration and growth process includes the steps of selection of transformant cells and shoots, rooting of transformant shoots and growth of the plantlets in soil. For maize cell culture and regeneration see generally, *The Maize Handbook*, Freeling and Walbot, Eds., Springer, New York (1994); *Corn and Corn Improvement*, 3rd edition, Sprague and Dudley Eds., American Society of Agronomy, Madison, Wisconsin (1988).

One of skill will recognize that after the recombinant expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

In vegetatively propagated crops, mature transgenic plants can be propagated by the taking of cuttings or by tissue culture techniques to produce multiple identical plants. Selection of desirable transgenics is made and new varieties are obtained and propagated vegetatively for commercial use. In seed propagated crops, mature transgenic plants can be self crossed to produce a homozygous inbred plant. The inbred plant produces seed containing the newly introduced heterologous nucleic acid. These seeds can be grown to

produce plants that would produce the selected phenotype, (*e.g.*, altered cell cycle content or composition).

Parts obtained from the regenerated plant, such as flowers, seeds, leaves, branches, fruit and the like are included in the invention, provided that these parts comprise cells
5 comprising the isolated nucleic acid of the present invention. Progeny and variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced nucleic acid sequences.

Transgenic plants expressing the selectable marker can be screened for transmission of the nucleic acid of the present invention by, for example, standard
10 immunoblot and DNA detection techniques. Transgenic lines are also typically evaluated on levels of expression of the heterologous nucleic acid. Expression at the RNA level can be determined initially to identify and quantitate expression-positive plants. Standard techniques for RNA analysis can be employed and include PCR amplification assays using oligonucleotide primers designed to amplify only the heterologous RNA templates and
15 solution hybridization assays using heterologous nucleic acid-specific probes. The RNA-positive plants can then analyzed for protein expression by Western immunoblot analysis using the specifically reactive antibodies of the present invention. In addition, *in situ* hybridization and immunocytochemistry according to standard protocols can be done using heterologous nucleic acid specific polynucleotide probes and antibodies, respectively, to
20 localize sites of expression within transgenic tissue. Generally, a number of transgenic lines are usually screened for the incorporated nucleic acid to identify and select plants with the most appropriate expression profiles.

A preferred embodiment of the invention is a transgenic plant that is homozygous for the added heterologous nucleic acid; *i.e.*, a transgenic plant that contains two added
25 nucleic acid sequences, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) a heterozygous transgenic plant that contains a single added heterologous nucleic acid, germinating some of the seed produced and analyzing the resulting plants produced for altered cell division relative to a control plant (*i.e.*, native, non-transgenic). Back-crossing
30 to a parental plant and out-crossing with a non-transgenic plant are also contemplated.

The present invention also relates to transgenic plants and plant tissue comprising transgenic plant cells according to the invention. Due to the (over)expression of a CCP molecule, *e.g.*, at developmental stages and/or in plant tissue in which they do not naturally occur, these transgenic plants may show various physiological, developmental and/or
35 morphological modifications in comparison to wild-type plants.

Therefore, part of this invention is the use of the CCP molecules to modulate the cell cycle and/or plant cell division and/or growth in plant cells, plant tissues, plant organs and/or whole plants. To the scope of the invention also belongs a method for influencing

the activity of CDKs such as CDC2a, or CDC2b, CKSs, CKIs, PLPs and KLPNTs in a plant cell by transforming the plant cell with a nucleic acid molecule according to the invention and/or manipulation of the expression of the molecule.

Furthermore, the invention also relates to a transgenic plant cell which contains
5 (preferably stably integrated into its genome) a nucleic acid molecule of the invention or part thereof, wherein the transcription and/or expression of the nucleic acid molecule or part thereof leads to reduction of the synthesis of a CCP. In a preferred embodiment, the reduction is achieved by an anti-sense, sense, ribozyme, co-suppression and/or dominant mutant effect. The reduction of the synthesis of a protein according to the invention in the
10 transgenic plant cells can result in an alteration in, *e.g.*, cell division. In transgenic plants comprising such cells this can lead to various physiological, developmental and/or morphological changes.

In yet another aspect, the invention relates to harvestable parts and to propagation material of the transgenic plants of the invention which either contain transgenic plant cells
15 expressing a nucleic acid molecule according to the invention or which contain cells which show a reduced level of the described protein. Harvestable parts can be in principle any useful parts of a plant, for example, flowers, pollen, seedlings, tubers, leaves, stems, fruit, seeds, roots etc. Propagation material includes, for example, seeds, fruits, cuttings, seedlings, tubers, rootstocks, and the like.

20

Transgenic Animals

As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include
25 non-human primates, sheep, dogs, cows, goats, chickens, amphibians, and the like. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a
30 non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous CCP gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing a CCP-encoding
35 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The CCP cDNA sequence of SEQ ID NO:1-66 or 228-239 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue

of a human CCP gene, such as a mouse or rat CCP gene, can be used as a transgene. Alternatively, a CCP gene homologue, such as another CCP family member, can be isolated based on hybridization to the CCP cDNA sequences of SEQ ID NO:1-66 or 228-239 (described further in subsection I above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to a CCP transgene to direct expression of a CCP protein to particular cells.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, both by Leder *et al.*, U.S. Patent No. 4,873,191 by Wagner *et al.* and in Hogan, B., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of a CCP transgene in its genome and/or expression of CCP mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding a CCP protein can further be bred to other transgenic animals carrying other transgenes.

V. Agricultural, Phytopharmaceutical and Pharmaceutical Compositions

The CCP nucleic acid molecules, CCP proteins, and anti-CCP antibodies (also referred to herein as "active compounds") of the invention can be incorporated into compositions useful in agriculture and in plant cell and tissue culture. Plant protection compositions can be prepared by conventional means commonly used for the application of, for example, herbicides and pesticides. For example, certain additives known to those skilled in the art stabilizers or substances which facilitate the uptake by the plant cell, plant tissue or plant may be used.

The CCP nucleic acid molecules, CCP proteins, and anti-CCP antibodies (also referred to herein as "active compounds") of the invention can also be incorporated into pharmaceutical compositions suitable for administration into animals. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is

contemplated. Supplementary active compounds can also be incorporated into the compositions.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a plant or subject by, for example, injection, local administration (see U.S. Patent 5,328,470) or by stereotactic injection (see *e.g.*, Chen *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The agricultural or pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the agricultural or pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The agricultural and pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

VI. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: a) agricultural uses (*e.g.*, to increase plant yield and to develop phytopharmaceuticals); b) screening assays; c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials); d) methods of treatment (*e.g.*, phytotherapeutic, therapeutic and prophylactic); e) transcriptomics; f) proteomics; g) metabolomics; h) ligandomics; and i) pharmacogenetics or pharmacogenomics. The isolated nucleic acid molecules of the invention can be used, for example, to express CCP protein (*e.g.*, via a recombinant expression vector in a host cell or in gene therapy applications), to detect CCP mRNA (*e.g.*, in a biological sample) or a genetic alteration in a CCP gene, and to modulate CCP activity, as described further below. The CCP proteins can be used to treat disorders characterized by insufficient or excessive production of a CCP substrate or production of CCP inhibitors. In addition, the CCP proteins can be used to screen for naturally occurring CCP substrates, to screen for drugs or compounds which modulate CCP activity, as well as to treat disorders characterized by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or aberrant activity compared to CCP wild type protein. Moreover, the anti-CCP antibodies of the invention can be used to detect and isolate CCP proteins, regulate the bioavailability of CCP proteins, and modulate CCP activity.

A. Agricultural Uses:

In another embodiment of the invention, a method is provided for modifying cell fate and/or plant development and/or plant morphology and/or biochemistry and/or physiology comprising the modification of expression in particular cells, tissues or organs of a plant, of a genetic sequence encoding a CCP, *e.g.*, a CCP operably connected with a
5 plant-operable promoter sequence.

Modulation of the expression in a plant of a CCP or a homologue, analogue or derivative thereof as defined in the present invention can produce a range of desirable phenotypes in plants, such as, for example, the modification of one or more morphological,
10 biochemical, or physiological characteristics including: (i) modification of the length of the G1 and/or the S and/or the G2 and/or the M phase of the cell cycle of a plant; (ii) modification of the G1/S and/or S/G2 and/or G2/M and/or M/G1 phase transition of a plant cell; (iii) modification of the initiation, promotion, stimulation or enhancement of cell division; (iv) modification of the initiation, promotion, stimulation or enhancement of
15 DNA replication; (v) modification of the initiation, promotion, stimulation or enhancement of seed set and/or seed size and/or seed development; (vi) modification of the initiation, promotion, stimulation or enhancement of tuber formation; (vii) modification of the initiation, promotion, stimulation or enhancement of fruit formation; (viii) modification of the initiation, promotion, stimulation or enhancement of leaf formation; (ix) modification
20 of the initiation, promotion, stimulation or enhancement of shoot initiation and/or development; (x) modification of the initiation, promotion, stimulation or enhancement of root initiation and/or development; (xi) modification of the initiation, promotion, stimulation or enhancement of lateral root initiation and/or development; (xii) modification of the initiation, promotion, stimulation or enhancement of nodule formation and/or nodule
25 function; (xiii) modification of the initiation, promotion, stimulation or enhancement of the bushiness of the plant; (xiv) modification of the initiation, promotion, stimulation or enhancement of dwarfism in the plant; (xv) modification of the initiation, promotion, stimulation or enhancement of senescence; (xvi) modification of stem thickness and/or strength characteristics and/or wind-resistance of the stem and/or stem length; (xvii)
30 modification of tolerance and/or resistance to biotic stresses such as pathogen infection; and (xviii) modification of tolerance and/or resistance to abiotic stresses such as drought stress or salt stress.

Methods to effect expression of a CCP or a homologue, analogue or derivative thereof as defined in the present invention in a plant cell, tissue or organ, include either the
35 introduction of the protein directly to a cell, tissue or organ such as by microinjection of ballistic means or, alternatively, introduction of an isolated nucleic acid molecule encoding the protein into the cell, tissue or organ in an expressible format. Methods to effect expression of a CCP or a homologue, analogue or derivative thereof as defined in the

current invention in whole plants include regeneration of whole plants from the transformed cells in which an isolated nucleic acid molecule encoding the protein was introduced in an expressible format.

The present invention clearly extends to any plant produced by the inventive method described herein, and any and all plant parts and propagules thereof. The present invention extends further to encompass the progeny derived from a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by the inventive method, the only requirement being that the progeny exhibits the same genotypic and/or phenotypic characteristic(s) as those characteristic(s) that (have) been produced in the parent by the performance of the inventive method.

By "cell fate and/or plant development and/or plant morphology and/or biochemistry and/or physiology" is meant that one or more developmental and/or morphological and/or biochemical and/or physiological characteristics of a plant is altered by the performance of one or more steps pertaining to the invention described herein. "Cell fate" includes the cell-type or cellular characteristics of a particular cell that are produced during plant development or a cellular process therefor, in particular during the cell cycle or as a consequence of a cell cycle process.

The term "plant development" or the term "plant developmental characteristic" or similar terms shall, when used herein, be taken to mean any cellular process of a plant that is involved in determining the developmental fate of a plant cell, in particular the specific tissue or organ type into which a progenitor cell will develop. Cellular processes relevant to plant development will be known to those skilled in the art. Such processes include, for example, morphogenesis, photomorphogenesis, shoot development, root development, vegetative development, reproductive development, stem elongation, flowering, and regulatory mechanisms involved in determining cell fate, in particular a process or regulatory process involving the cell cycle.

The term "plant morphology" or the term "plant morphological characteristic" or similar term will, when used herein, be understood by those skilled in the art to include the external appearance of a plant, including any one or more structural features or combination of structural features thereof. Such structural features include the shape, size, number, position, color, texture, arrangement, and patternation of any cell, tissue or organ or groups of cells, tissues or organs of a plant, including the root, stem, leaf, shoot, petiole, trichome, flower, petal, stigma, style, stamen, pollen, ovule, seed, embryo, endosperm, seed coat, aleurone, fibre, fruit, cambium, wood, heartwood, parenchyma, aerenchyma, sieve element, phloem or vascular tissue.

The term "plant biochemistry" or the term "plant biochemical characteristic" or similar term will, when used herein, be understood by those skilled in the art to include the metabolic and catalytic processes of a plant, including primary and secondary metabolism

and the products thereof, including any small molecules, macromolecules or chemical compounds, such as but not limited to starches, sugars, proteins, peptides, enzymes, hormones, growth factors, nucleic acid molecules, celluloses, hemicelluloses, calloses, lectins, fibres, pigments such as anthocyanins, vitamins, minerals, micronutrients, or
5 macronutrients, that are produced by plants.

The term "plant physiology" or the term "plant physiological characteristic" or similar term will, when used herein, be understood to include the functional processes of a plant, including developmental processes such as growth, expansion and differentiation, sexual development, sexual reproduction, seed set, seed development, grain filling, asexual
10 reproduction, cell division, dormancy, germination, light adaptation, photosynthesis, leaf expansion, fibre production, secondary growth or wood production, amongst others; responses of a plant to externally-applied factors such as metals, chemicals, hormones, growth factors, environment and environmental stress factors (*e.g.*, anoxia, hypoxia, high temperature, low temperature, dehydration, light, daylength, flooding, salt, heavy metals,
15 amongst others), including adaptive responses of plants to said externally-applied factors.

The CCP molecules of the present invention are useful in agriculture. The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used to modulate the protein levels or activity of a protein involved in the cell cycle, *e.g.*, proteins involved in the G1/S and/or the G2/M transition in the cell cycle due to
20 environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as a pathogen attack.

Thus, the CCP molecules of the present invention may be used to modulate, *e.g.*, enhance, crop yields; modulate, *e.g.*, attenuate, stress, *e.g.* heat or nutrient deprivation; modulate tolerance to pests and diseases; modulate plant architecture; modulate plant
25 quality traits; or modulate plant reproduction and seed development.

The CCP molecules of the present invention may also be used to modulate endoreduplication in storage cells, storage tissues, and/or storage organs of plants or parts thereof. The term "endoreduplication" includes recurrent DNA replication without consequent mitosis and cytokinesis. Preferred target storage organs and parts thereof for
30 the modulation of endoreduplication are, for example, seeds (such as from cereals, oilseed crops), roots (such as in sugar beet), tubers (such as in potatoes) and fruits (such as in vegetables and fruit species). Increased endoreduplication in storage organs, and parts thereof, correlates with enhanced storage capacity and, thus, with improved yield. In another embodiment of the invention, the endoreduplication of a whole plant is modulated.

35

B. Screening Assays:

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,

peptidomimetics, small molecules or other drugs) which bind to CCP proteins, have a stimulatory or inhibitory effect on, for example, CCP expression or CCP activity, or have a stimulatory or inhibitory effect on, for example, the expression or activity of a CCP substrate.

5 In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a CCP protein or polypeptide or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a CCP protein or polypeptide or biologically active portion thereof, *e.g.*, modulate the ability of CCP to
10 interact with its cognate ligand. The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography
15 selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.*
20 (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992)
25 *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner USP 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith (1990) *Science* 249:386-390); (Devlin (1990) *Science* 249:404-406); (Cwirla *et al.* (1990) *Proc. Natl. Acad. Sci.* 87:6378-6382); (Felici (1991) *J. Mol. Biol.* 222:301-310);
30 (Ladner *supra.*).

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a CCP target molecule (*e.g.*, a plant cyclin dependent kinase) with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the CCP target molecule. Determining the ability of the test
35 compound to modulate the activity of a CCP target molecule can be accomplished, for example, by determining the ability of the CCP protein to bind to or interact with the CCP target molecule, or by determining the ability of the target molecule, *e.g.*, the plant cyclin dependent kinase, to phosphorylate a protein.

The ability of the target molecule, *e.g.*, the plant cyclin dependent kinase, to phosphorylate a protein can be determined by, for example, an *in vitro* kinase assay. Briefly, a protein can be incubated with the target molecule, *e.g.*, the plant cyclin dependent kinase, and radioactive ATP, *e.g.*, [γ - ^{32}P] ATP, in a buffer containing MgCl_2 and MnCl_2 , *e.g.*, 10 mM MgCl_2 and 5 mM MnCl_2 . Following the incubation, the immunoprecipitated protein can be separated by SDS-polyacrylamide gel electrophoresis under reducing conditions, transferred to a membrane, *e.g.*, a PVDF membrane, and autoradiographed. The appearance of detectable bands on the autoradiograph indicates that the protein has been phosphorylated. Phosphoaminoacid analysis of the phosphorylated substrate can also be performed in order to determine which residues on the protein are phosphorylated. Briefly, the radiophosphorylated protein band can be excised from the SDS gel and subjected to partial acid hydrolysis. The products can then be separated by one-dimensional electrophoresis and analyzed on, for example, a phosphoimager and compared to ninhydrin-stained phosphoaminoacid standards.

Determining the ability of the CCP protein to bind to or interact with a CCP target molecule can be accomplished by determining direct binding. Determining the ability of the CCP protein to bind to or interact with a CCP target molecule can be accomplished, for example, by coupling the CCP protein with a radioisotope or enzymatic label such that binding of the CCP protein to a CCP target molecule can be determined by detecting the labeled CCP protein in a complex. For example, CCP molecules, *e.g.*, CCP proteins, can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, CCP molecules can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

It is also within the scope of this invention to determine the ability of a compound to modulate the interaction between CCP and its target molecule, without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of CCP with its target molecule without the labeling of either CCP or the target molecule. McConnell, H. M. *et al.* (1992) *Science* 257:1906-1912. As used herein, a "microphysiometer" (*e.g.*, Cytosensor) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between compound and receptor.

In a preferred embodiment, determining the ability of the CCP protein to bind to or interact with a CCP target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*e.g.*, intracellular Ca^{2+} ,

diacylglycerol, IP₃, etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a target-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, chloramphenicol acetyl transferase), or detecting a target-regulated cellular response.

5 In yet another embodiment, an assay of the present invention is a cell-free assay in which a CCP protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to bind to the CCP protein or biologically active portion thereof is determined. Binding of the test compound to the CCP protein can be determined either directly or indirectly as described above. In a preferred embodiment,
10 the assay includes contacting the CCP protein or biologically active portion thereof with a known compound which binds CCP to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a CCP protein, wherein determining the ability of the test compound to interact with a CCP protein comprises determining the ability of the test compound to preferentially bind to
15 CCP or biologically active portion thereof as compared to the known compound.

In another embodiment, the assay is a cell-free assay in which a CCP protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the CCP protein or biologically active portion thereof is determined. Determining the ability of the test
20 compound to modulate the activity of a CCP protein can be accomplished, for example, by determining the ability of the CCP protein to bind to a CCP target molecule by one of the methods described above for determining direct binding. Determining the ability of the CCP protein to bind to a CCP target molecule can also be accomplished using a technology such as real-time Biomolecular Interaction Analysis (BIA). Sjolander, S. and
25 Urbaniczky, C. (1991) *Anal. Chem.* 63:2338-2345 and Szabo *et al.* (1995) *Curr. Opin. Struct. Biol.* 5:699-705. As used herein, "BIA" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the optical phenomenon of surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

30 In an alternative embodiment, determining the ability of the test compound to modulate the activity of a CCP protein can be accomplished by determining the ability of the CCP protein to further modulate the activity of a CCP target molecule (*e.g.*, a CCP mediated signal transduction pathway component). For example, the activity of the effector molecule on an appropriate target can be determined, or the binding of the effector
35 to an appropriate target can be determined as previously described.

In yet another embodiment, the cell-free assay involves contacting a CCP protein or biologically active portion thereof with a known compound which binds the CCP protein to form an assay mixture, contacting the assay mixture with a test compound, and

determining the ability of the test compound to interact with the CCP protein, wherein determining the ability of the test compound to interact with the CCP protein comprises determining the ability of the CCP protein to preferentially bind to or modulate the activity of a CCP target molecule.

5 The cell-free assays of the present invention are amenable to use of both soluble and/or membrane-bound forms of proteins (*e.g.*, CCP proteins or biologically active portions thereof). In the case of cell-free assays in which a membrane-bound form a protein is used it may be desirable to utilize a solubilizing agent such that the membrane-bound form of the protein is maintained in solution. Examples of such solubilizing agents
10 include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-
15 dodecyl=N,N-dimethyl-3-ammonio-1-propane sulfonate.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either CCP or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to a CCP protein, or
20 interaction of a CCP protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example,
25 glutathione-S-transferase/ CCP fusion proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the test compound or the test compound and either the non-adsorbed target protein or CCP protein, and the mixture incubated under conditions conducive to complex formation (*e.g.*, at
30 physiological conditions for salt and pH). Following incubation, the beads or microtitre plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of CCP binding or activity determined using standard techniques.

35 Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a CCP protein or a CCP target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated CCP protein or target molecules can be prepared from biotin-NHS (N-hydroxy-

succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with CCP protein or target molecules but which do not interfere with binding of the CCP protein to its target molecule
5 can be derivatized to the wells of the plate, and unbound target or CCP protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the CCP protein or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the
10 CCP protein or target molecule.

In another embodiment, modulators of CCP expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of CCP mRNA or protein in the cell is determined. The level of expression of CCP mRNA or protein in the presence of the candidate compound is compared to the level of expression of CCP
15 mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of CCP expression based on this comparison. For example, when expression of CCP mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of CCP mRNA or protein expression.
20 Alternatively, when expression of CCP mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of CCP mRNA or protein expression. The level of CCP mRNA or protein expression in the cells can be determined by methods described herein for detecting CCP mRNA or protein.

25 In yet another aspect of the invention, the CCP proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J. Biol. Chem.* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins, which bind to or interact
30 with CCP ("CCP-binding proteins" or "CCP-bp") and are involved in CCP activity. Such CCP-binding proteins are also likely to be involved in the propagation of signals by the CCP proteins or CCP targets as, for example, downstream elements of a CCP-mediated signaling pathway. Alternatively, such CCP-binding proteins are likely to be CCP inhibitors. Alternatively, a mammalian two-hybrid system can be used which includes e.g.
35 a chimeric green fluorescent protein encoding reporter gene (Shioda *et al.* 2000, *Proc. Natl. Acad. Sci. USA* 97, 5520-5224). Yet another alternative consists of a bacterial two-hybrid system using e.g. *HIS* as reporter gene (Joung *et al.* 2000, *Proc. Natl. Acad. Sci. USA* 97, 7382-7387).

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for a CCP protein is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a CCP-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the CCP protein.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate plant or animal model. For example, an agent identified as described herein (e.g., a CCP modulating agent, an antisense CCP nucleic acid molecule, a CCP-specific antibody, or a CCP-binding partner) can be used in a plant or animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in a plant or animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for the agricultural and therapeutic uses described herein.

C. Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; identify an individual from a minute biological sample (tissue typing); and aid in forensic identification of a biological sample. Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the CCP nucleotide sequences, described herein, can be used to map the location of the CCP genes on a chromosome. The mapping of the CCP sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, CCP genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the CCP nucleotide sequences. Computer analysis of the CCP sequences can be used to predict primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of cell hybrids containing individual plant or human chromosomes. Only those hybrids containing the plant or human gene corresponding to the CCP sequences will yield an amplified fragment.

Other mapping strategies which can similarly be used to map a CCP sequence to its chromosome include *in situ* hybridization (described in Fan, Y. *et al.* (1990) *Proc. Natl. Acad. Sci. USA*, 87:6223-27), pre-screening with labeled flow-sorted chromosomes, and pre-selection by hybridization to chromosome specific cDNA libraries.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical such as colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases will suffice to get good results at a reasonable amount of time. For a review of this technique, see Verma *et al.*, *Human Chromosomes: A Manual of Basic Techniques* (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. (Such data are found, for example, in V. McKusick, *Mendelian Inheritance in Man*, available on-line through Johns Hopkins University Welch Medical Library). The relationship between a gene and a disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, for example, Egeland, J. *et al.* (1987) *Nature*, 325:783-787.

Moreover, differences in the DNA sequences between plants affected and unaffected with a disease associated with the CCP gene, can be determined. If a mutation

is observed in some or all of the affected plants but not in any unaffected plants, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected plants generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several plants can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

D. Predictive Medicine:

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining CCP protein and/or nucleic acid expression as well as CCP activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant CCP expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with CCP protein, nucleic acid expression or activity. For example, mutations in a CCP gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with CCP protein, nucleic acid expression or activity.

Another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of CCP in clinical trials.

E. Methods of Treatment:

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant CCP expression or activity. With regards to both prophylactic and therapeutic methods of treatment, such treatments may be specifically tailored or modified, based on knowledge obtained from the field of pharmacogenomics. "Pharmacogenomics", as used herein, refers to the application of genomics technologies such as gene sequencing, statistical genetics, and gene expression analysis to drugs in clinical development and on the market. More specifically, the term refers the study of how a patient's genes determine his or her response to a drug (*e.g.*, a patient's "drug response phenotype", or "drug response genotype".) Thus, another aspect of the invention provides methods for tailoring an individual's prophylactic or therapeutic treatment with either the CCP molecules of the

present invention or CCP modulators according to that individual's drug response genotype. Pharmacogenomics allows a clinician or physician to target prophylactic or therapeutic treatments to patients who will most benefit from the treatment and to avoid treatment of patients who will experience toxic drug-related side effects.

5

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application, as well as the Figures and the Sequence Listing are incorporated herein by reference.

EXAMPLES

5 **EXAMPLE 1: IDENTIFICATION OF PLANT CCP POLYPEPTIDES USING THE TWO HYBRID SYSTEM WITH CDC2B AS A BAIT**

A two-hybrid screening was performed using as bait a fusion between the GAL4 DNA-binding domain and one of the following: CDC2bAt.N161 (GenBank accession number D10851; residue Asp161 converted into Asn161); CKS1At (GenBank accession
10 number AJ000016); E2Fa (=E2F5) (GenBank accession number AJ294534) dimerization domain (226-356aa; SEQ ID NO:205); CKI4 (SEQ ID NO:264); PLP1 (GenBank accession number T01601); KLPNT1 (GenBank accession number AB011479; protein ID number BAB11568) motor domain (36-508 aa); KLPNT1 (GenBank accession number AB011479; protein ID number BAB11568) stalk domain (427-867 aa); KLPNT2=TH65
15 (GenBank accession number AJ001729) neck domain (3-186 aa); KLPNT2=TH65 (GenBank accession number AJ001729) stalk domain (73-608 aa); E2Fb (=E2F3) (GenBank accession number AJ294533) N-terminal domain (1-385 aa; SEQ ID NO:206), respectively

CDC2bAt.N161 is a dominant negative form of the CDC2bAt protein. The D161
20 residue in CDC2bAt is crucial for ATP binding and, thus, the mutation of this residue results in an inactive kinase. The interactions between this mutated CDK and its substrates and regulatory proteins are also more stabilised as a result of this mutation.

In yeast the PHO genes are part of a complex regulatory network linking phosphate availability with the expression of phosphatases. When phosphate levels are high the
25 PHO80/PHO85 cyclin/CDK complex phosphorylates a transcription factor. This transcription factor of phosphatase genes thereby becomes inactive. The *S. cerevisiae* PHO85 protein can interact with the G1 specific cyclins PCL1 and PCL2 (close homologues to the PHO80). In a yeast strain deficient for the G1 cyclins CLN1 and CLN2, PHO80 is required for G1 progression. This result suggests that PHO85 is involved in a
30 regulatory pathway that links the nutrient status of the cell with cell division activity. The five PLP of *A. thaliana* show similarity to the yeast cyclin-like PHO80 gene.

Kinesins use the cytoskeleton to move around vesicles, organelles, chromosomes and the like in the cell. They can also be involved in spindle formation. Kinesins consist of three functional unrelated domains: the motor domain (involved in microtubule binding;
35 contains the ATPase domain), the stalk region (involved in homo- or heterodimerisation of the kinesins), and the tail (involved in the interaction with the 'substrates' of the kinesin). Two hybrid screens were performed using different parts of two-kinesin-related proteins (KLPNT1 and KLPNT2 (being more than 80% identical to KLPNT1). Other information

obtained by the two hybrid approach is the dimerization of the kinesins: the KLPNT1 and KLPNT2 interact (stalks and stalks-tail) with and between themselves.

Vectors and strains used were provided with the Matchmaker Two-Hybrid System (Clontech, Palo Alto, CA). The bait was constructed by inserting the CDC2bAt.N161 (GenBank accession number D10851; residue Asp161 converted into Asn161); CKS1At (GenBank accession number AJ000016); E2Fa (=E2F5) (GenBank accession number AJ294534) dimerization domain (226-356aa; SEQ ID NO:205); CKI4 (SEQ ID NO:264); PLP1 (GenBank accession number T01601); KLPNT1 (GenBank accession number AB011479; protein ID number BAB11568) motor domain (36-508 aa); KLPNT1 (GenBank accession number AB011479; protein ID number BAB11568) stalk domain (427-867 aa); KLPNT2=TH65 (GenBank accession number AJ001729) neck domain (3-186 aa); KLPNT2=TH65 (GenBank accession number AJ001729) stalk domain (73-608 aa); E2Fb (=E2F3) (GenBank accession number AJ294533) N-terminal domain (1-385 aa; SEQ ID NO:206), respectively, into the pGBT9 vector. Bait vectors were constructed by introducing the PCR fragment created from the corresponding cDNA using primers to incorporate *Eco*RI and *Bam*HI restriction enzyme sites. The PCR fragment was cut with *Eco*RI and *Bam*HI and cloned into the *Eco*RI and *Bam*HI sites of pGBT9, resulting in the desired plasmid. The GAL4 activation domain cDNA fusion library was constructed as described in De Veylder *et al* 1999, 208(4) p453-62 from mRNA of *Arabidopsis thaliana* cell suspensions harvested at various growing stages: early exponential, exponential, early stationary, and stationary phase.

For the screening a 1-liter culture of the *Saccharomyces cerevisiae* strain HF7c (*MATa ura3-52 his3-200 ade2-101 lys2-801 trp1-901 leu2-3,112 gal4-542 gal80-538 LYS2::GAL1_{UAS}-GAL1_{TATA}-HIS3 URA3::GAL4_{17mers}(3x)-CYC1_{TATA}-LacZ*) was sequentially transformed with the bait plasmid and 20µg DNA of the library using the lithium acetate method (Geitz *et al.* (1992) *supra*). To estimate the number of independent cotransformants, 1/1000 of the transformation mix was plated on Leu- and Trp- medium. The rest of the transformation mix was plated on medium to select for histidine prototrophy (Trp-, Leu-, His-). After 5 days of growth at 30°C, the colonies larger than 2 mm were streaked on histidine-lacking medium. At total for each screening at least 10⁷ independent cotransformants were screened for their ability to grow on histidine free medium. Of the His⁺ colonies the activation domain plasmids were isolated as described (Hoffman and Winston, 1987, *Gene* 57, 267-272). The hybriZAP™ inserts were PCR amplified and the PCR fragments were digested with *Alu*I and fractionized on a 2% agarose gel. Plasmid DNA of which the inserts gave rise to different restriction patterns were electroporated into *Escherichia coli* XL1-Blue, and the DNA sequence of the inserts was determined. Extracted DNA was also used to retransform HF7c to test the specificity of the interaction.

Using the foregoing technique, 61 cDNAs were identified, their sequences were determined and found to contain open reading frames termed CCP1 through CCP61 (Figures 1-61).

5 **EXAMPLE 2: EXTENSION OF CCP ENCODING POLYNUCLEOTIDES
 TO FULL LENGTH OR TO RECOVER REGULATORY
 ELEMENTS**

The CCP encoding nucleic acid sequences (SEQ ID NO:1-66 or 228-239) are used to design oligonucleotide primers for extending a partial nucleotide sequence to full length
10 or for obtaining 5' sequences from genomic or cDNA libraries. One primer is synthesized to initiate extension in the antisense direction (XLR) and the other is synthesized to extend sequence in the sense direction (XLF). Primers allow the extension of the known CCP encoding sequence "outward" generating amplicons containing new, unknown nucleotide sequence for the region of interest. The initial primers are designed from the cDNA using
15 OLIGO® 4.06 Primer Analysis Software (National Biosciences), or another appropriate program, to be preferably 22-30 nucleotides in length, to have a GC content of preferably 50% or more, and to anneal to the target sequence at temperatures preferably about 68°-72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations is avoided. The original, selected cDNA libraries, prepared from
20 mRNA isolated from actively dividing cells or a plant genomic library are used to extend the sequence; the latter is most useful to obtain 5' upstream regions. If more extension is necessary or desired, additional sets of primers are designed to further extend the known region.

Sense XLF primers can also be designed based on publicly available genomic
25 sequences. GENEMARK.hmm (hidden markov model) version 2.2a software (default parameters) can e.g. be used to predict open reading frames. The 5' end of the predicted open reading frame is then subsequently used to design the sense XLF primer. Said XLF primer and the appropriate XLR primer are then used in an RT-PCR (reverse transcription-polymerase chain reaction) reaction to amplify the predicted cDNA. The resulting PCR
30 product is cloned in a suitable vector and subjected to DNA sequence analysis to verify the prediction.

Primers used to amplify coding regions of the CCPs of the invention are designed such that the PCR product can be cloned in the pDONR201 vector (Gateway™ cloning system, Invitrogen). Thus, a sense primer has the attB1 site (SEQ ID NO:246) at its 5' end.
35 For current purposes, the attB1 site is followed by a consensus Kozak sequence (SEQ ID NO:247; Kozak (1989) *J Cell Biol* 108:229-241; Lütck *et al.* (1987) *EMBO J* 6:43-48). The 3' end of the sense primer comprises the gene-specific parts as indicated in Figures 1-46. An antisense primer has at the 5' end the attB2 site (SEQ ID NO:248) followed by the

inverse complement of the gene/coding region of interest as indicated in Figures 1-46. Primers used for CCP amplification by PCR are given with their SEQ ID NOs in Table 3. The sequence of cloned CCP PCR products was or is determined using the sense primer prm1024 (SEQ ID NO:265) and the antisense primer prm1025 (SEQ ID NO:266).

5

TABLE III:

CCP Molecule	PCR primers sense + antisense	sense primer SEQ ID NO:	antisense primer SEQ ID NO:
CCP1	prm0733 + prm0734	133	134
CCP2	prm0663 + prm0664	135	136
CCP3	prm0705 + prm0706	137	138
CCP4	prm0659 + prm0660	139	140
CCP5	prm0749 + prm0750	141	142
CCP6	prm0707 + prm 0708	143	144
CCP7/8	prm0657 + prm0658	145	146
CCP9	prm0582 + prm0583	147	148
CCP10	prm0671 + prm0672	149	150
CCP11	prm0729 + prm0730	151	152
CCP12+ CCP13	prm1676 + prm1677	153	154
CCP14	prm0701 + prm0702	155	156
CCP15	prm0445 + prm0446	157	158
CCP16	prm0321 + prm0322	159	160
CCP17	prm0632 + prm0633	161	162
CCP18	prm0488 + prm0489	163	164
CCP19	prm0661 + prm0662	165	166
CCP20+ CCP21	prm0709 + prm0710	167	168
CCP22	prm0711 + prm0712	169	170
CCP23	prm0819 + prm0820	171	172
CCP24	prm0739 + prm0740	173	174
CCP25	prm0741 + prm0742	175	176
CCP26	prm0703 + prm0704	177	178
CCP27	prm0817 + prm0818	179	180
CCP28	prm0713 + prm0714	181	182
CCP29	/	/	/
CCP30	prm0480 + prm0481	183	184
CCP31	prm0737 + prm0738	185	186
CCP32	prm1493 + prm1494	187	188
CCP33	prm0319 + prm0320	189	190
CCP34	prm1377 + prm1378	191	192

CCP35	prm1381 + prm1382	193	194
CCP36	/	/	/
CCP37	prm1379 + prm1380	195	196
CCP38	prm1383 + prm1384	197	198

By following the instructions for the XL-PCR kit (Perkin Elmer) and thoroughly mixing the enzyme and reaction mix, high fidelity amplification is obtained. Beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, PCR is performed using the Peltier Thermal Cycle (PTC200; MJ Research, Watertown MA) and the following parameters:

- | | |
|------------|-------------------------------------------|
| Step 1 | 94°C for 1 min (initial denaturation) |
| Step 2 | 65°C for 1 min |
| 10 Step 3 | 68°C for 6 min |
| Step 4 | 94° for 15 sec |
| Step 5 | 65°C for 1 min |
| Step 6 | 68°C for 7 min |
| Step 7 | Repeat steps 4-6 for 15 additional cycles |
| 15 Step 8 | 94°C for 15 sec |
| Step 9 | 65°C for 1 min |
| Step 10 | 68°C for 7:15 min |
| Step 11 | Repeat step 8-10 for 12 cycles |
| Step 12 | 72°C for 8 min |
| 20 Step 13 | 4°C (and holding) |

A 5-10 µl aliquot of the reaction mixture is analyzed by electrophoresis on a low concentration (about 0.6-0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Bands thought to contain the largest products were selected and cut out of the gel. Further purification involves using a commercial gel extraction method such as QIAQuick™ (QIAGEN Inc). After recovery of the DNA, Klenow enzyme was used to trim single-stranded, nucleotide overhangs creating blunt ends which facilitate religation and cloning. After ethanol precipitation, the products are redissolved in 13 µl of ligation buffer, 1µl T4-DNA ligase (15 units) and 1 µl T4 polynucleotide kinase are added, and the mixture is incubated at room temperature for 2-3 hours or overnight at 16°C. Competent *E. coli* cells (in 40 µl of appropriate media) are transformed with 3 µl of ligation mixture and cultured in 80 µl of SOC medium (Sambrook, supra). After incubation for one hour at 37°C, the whole transformation mixture is plated on Luria Bertani (LB)-agar (Sambrook, supra) containing 2xCarb. The

following day, several colonies are randomly picked from each plate and cultured in 150 μ l of liquid LB/2xCarb medium placed in an individual well of an appropriate, commercially-available, sterile 96-well microtiter plate. The following day, 5 μ l of each overnight culture is transferred into a non-sterile 96-well plate and after dilution 1:10 with water, 5 μ l of each sample is transferred into a PCR array. For PCR amplification, 18 μ l of concentrated PCR reaction mix (3.3x) containing 4 units of 4Tth DNA polymerase, a vector primer and both of the gene specific primers used for the extension reaction are added to each well. Amplification is performed using the following conditions:

- | | | |
|----|--------|----------------------------------------------|
| 10 | Step 1 | 94°C for 60 sec |
| | Step 2 | 94°C for 20 sec |
| | Step 3 | 55°C for 30 sec |
| | Step 4 | 72°C for 90 sec |
| | Step 5 | Repeat steps 2-4 for an additional 29 cycles |
| 15 | Step 6 | 72°C for 180 sec |
| | Step 7 | 4°C (and holding) |

Aliquots of the PCR reactions are run on agarose gels together with molecular weight markers. The sizes of the PCR products are compared to the original partial cDNAs, and appropriate clones are selected, ligated into plasmid and sequenced.

EXAMPLE 3: EXPRESSION OF RECOMBINANT CCP PROTEINS IN TRANSGENIC PLANTS

In this example, the CCP molecules of the present invention were expressed in a 35S expression vector in transgenic plants. The CCP molecules of this invention were cloned using standard cloning procedures between a suitable promoter, *e.g.* the *CaMV35S* promoter or any promoter from *e.g.* Table II, and a suitable terminator, *e.g.* the NOS 3' untranslated region. The resulting recombinant gene is subsequently cloned in a suitable binary vector and the resulting plant transformation vector is then transferred to *Agrobacterium tumefaciens*. *Arabidopsis thaliana* is transformed with this *Agrobacterium* applying the in planta flower-dip transformation method (Clough and Bent, *Plant J.* 16:735-743, 1998). Transgenic plant lines are selected on a growth medium containing the suitable selection agent (*e.g.*, kanamycin or Basta) or on the basis of scoring the expression of a screenable marker (*e.g.*, luciferase, green fluorescent protein).

For tissue-specific expression, the CCP gene can also be expressed under control of the minimal 35S promoter containing UAS elements. These UAS elements are sites for transcriptional activation by the GAL4-VP16 fusion protein. The GAL4-VP16 fusion

protein in turn is expressed under control of a tissue-specific promoter. The UAS-CCP construct and the GAL4-VP16 construct are combined by co-transformation of both constructs, subsequent transformation of single constructs or by sexual cross of lines that contain the single constructs. The advantage of this two-component system is that a wide array of tissue-specific expression patterns can be generated for a specific transgene, by simply crossing selected parent lines expressing the UAS-CCP construct with various tissue-specific GAL4-VP16 lines. A tissue-specific promoter/CCP combination that gives a desired phenotype can subsequently be recloned in a single expression vector, to avoid stacking of transgene constructs in commercial lines.

Primary transformants are characterized by Northern and Western blotting using 1-4 week old plantlets. Expression levels were compared with those of non-transformed (control) plants.

EXAMPLE 4: DOWNREGULATION OF TARGET CCP GENES IN TRANSGENIC PLANTS

Plant genes can be specifically downregulated by antisense and co-suppression technologies. These technologies are based on the synthesis of antisense transcripts, complementary to the mRNA of a given CCP gene. There are several methods described in literature, that increase the efficiency of this downregulation, for example to express the sense strand with introduced inverted repeats, rather than the antisense strand. The constructs for downregulation of target genes are made similarly as those for expression of recombinant proteins, *i.e.*, they are fused to promoter sequences and transcription termination sequences (see example 3). Promoters used for this purpose are constitutive promoters as well as tissue-specific promoters.

EXAMPLE 5: AGROBACTERIUM-MEDIATED RICE TRANSFORMATION

Mature dry seeds of the rice japonica cultivars Nipponbare or Taipei 309 are dehusked, sterilised and germinated on a medium containing 2,4-D (2,4-dichlorophenoxyacetic acid). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli are excised and propagated on the same medium. Selected embryogenic calluses are then co-cultivated with *Agrobacterium*. Widely used *Agrobacterium* strains such as LBA4404 or C58 harbouring binary T-DNA vectors can be used. The *hpt* gene in combination with hygromycin is suitable as a selectable marker system but other systems can be used. Co-cultivated callus is grown on 2,4-D-containing medium for 4 to 5 weeks in the dark in the presence of a suitable concentration of the selective agent. During this period, rapidly growing resistant callus islands develop. After

-91-

transfer of this material to a medium with a reduced concentration of 2,4-D and incubation in the light, the embryogenic potential is released and shoots develop in the next four to five weeks. Shoots are excised from the callus and incubated for one week on an auxin-containing medium from which they can be transferred to the soil. Hardened shoots are grown under high humidity and short days in a phytotron. Seeds can be harvested three to five months after transplanting. The method yields single locus transformants at a rate of over 50 % (Aldemita and Hodges (1996) *Planta* 199:612-617; Chan *et al.* (1993) *Plant Mol. Biol.* 22: 491-506 ; Hiei *et al.* (1994) *Plant J.* 6 :271-282).

10 **EXAMPLE 6: EXPRESSION OF RECOMBINANT CCP PROTEINS IN BACTERIAL CELLS**

In this example, the CCP molecules of the present invention are expressed as a recombinant glutathione-S-transferase (GST) fusion polypeptide in *E. coli* and the fusion polypeptide is isolated and characterized. Specifically, CCP molecules are fused to GST and this fusion polypeptide is expressed in *E. coli*, *e.g.*, strain PEB199. Expression of the GST-CCP fusion protein in PEB199 is induced with IPTG. The recombinant fusion polypeptide is purified from crude bacterial lysates of the induced PEB199 strain by affinity chromatography on glutathione beads. Using polyacrylamide gel electrophoretic analysis of the polypeptide purified from the bacterial lysates, the molecular weight of the resultant fusion polypeptide is determined.

EXAMPLE 7: EXPRESSION OF RECOMBINANT CCP PROTEINS IN COS CELLS

25

To express the CCP gene of the present invention in COS cells, the pcDNA/Amp vector by Invitrogen Corporation (San Diego, CA) is used. This vector contains an SV40 origin of replication, an ampicillin resistance gene, an *E. coli* replication origin, a CMV promoter followed by a polylinker region, and an SV40 intron and polyadenylation site. A DNA fragment encoding the entire CCP protein and an HA tag (Wilson *et al.* (1984) *Cell* 37:767) or a FLAG tag fused in-frame to its 3' end of the fragment is cloned into the polylinker region of the vector, thereby placing the expression of the recombinant protein under the control of the CMV promoter.

To construct the plasmid, the CCP DNA sequence is amplified by PCR using two primers. The 5' primer contains the restriction site of interest followed by approximately twenty nucleotides of the CCP coding sequence starting from the initiation codon; the 3' end sequence contains complementary sequences to the other restriction site of interest, a translation stop codon, the HA tag or FLAG tag and the last 20 nucleotides of the CCP

coding sequence. The PCR amplified fragment and the pCDNA/Amp vector are digested with the appropriate restriction enzymes and the vector is dephosphorylated using the CIAP enzyme (New England Biolabs, Beverly, MA). Preferably the two restriction sites chosen are different so that the Kinase and/or Phosphatase gene is inserted in the correct orientation. The ligation mixture is transformed into *E. coli* cells (strains HB101, DH5a, SURE, available from Stratagene Cloning Systems, La Jolla, CA, can be used), the transformed culture is plated on ampicillin media plates, and resistant colonies are selected. Plasmid DNA is isolated from transformants and examined by restriction analysis for the presence of the correct fragment.

COS cells are subsequently transfected with the CCP-pcDNA/Amp plasmid DNA using the calcium phosphate or calcium chloride co-precipitation methods, DEAE-dextran-mediated transfection, lipofection, or electroporation. Other suitable methods for transfecting host cells can be found in Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. The expression of the CCP polypeptide is detected by radiolabelling (^{35}S -methionine or ^{35}S -cysteine available from NEN, Boston, MA, can be used) and immunoprecipitation (Harlow, E. and Lane, D. *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1988) using an HA specific monoclonal antibody. Briefly, the cells are labelled for 8 hours with ^{35}S -methionine (or ^{35}S -cysteine). The culture media are then collected and the cells are lysed using detergents (RIPA buffer, 150 mM NaCl, 1% NP-40, 0.1% SDS, 0.5% DOC, 50 mM Tris, pH 7.5). Both the cell lysate and the culture media are precipitated with an HA specific monoclonal antibody. Precipitated polypeptides are then analyzed by SDS-PAGE.

Alternatively, DNA containing the Kinase and/or Phosphatase coding sequence is cloned directly into the polylinker of the pCDNA/Amp vector using the appropriate restriction sites. The resulting plasmid is transfected into COS cells in the manner described above, and the expression of the CCP polypeptide is detected by radiolabelling and immunoprecipitation using a CCP specific monoclonal antibody.

EXAMPLE 8: *IN VITRO* PHOSPHORYLATION OF CDC2bDN-IC26M BY PLANT CDKs.

The CDC2bDN-IC26M coding region (SEQ ID NO:4) was amplified by PCR with *Pfu* polymerase (Stratagene, La Jolla, CA). The PCR product was subcloned into pET19b (Novagen, Madison, WI), to obtain CDC2bDN-IC26MpET19b. The CDC2bDN-IC26M gene is located downstream of a T7lac promoter, in frame with a sequence encoding a 10-

histidine tag followed by an enterokinase recognition site. *Escherichia coli* BL21(DE3) cells (Novagen) containing the CDC2bDN-IC26MpET19b plasmid were grown at 37 °C in M9 medium (Sambrook and Russel, Molecular Cloning, A Laboratory Manual, 3rd Edition, CSHL Press, CSH New York, 2001), supplemented with 100 µg/ml of ampicillin, to
5 obtain a cell density corresponding to an A600 of 0.6. Subsequently, expression of the CDC2bDN-IC26M gene was induced by addition of 0.4 mM isopropyl β-D-thiogalactoside, and culture was continued for 4 h at 30 °C.

Cells were collected in lysis buffer containing 50 mM sodium phosphate buffer, pH 8.0, 300 mM NaCl, 0.1% Triton X-100, and 1 mM phenylmethylsulfonyl fluoride (PMSF)
10 and were lysed on ice by sonication. The extract was clarified by centrifugation for 20 minutes at 20,000 × g. The crude extract was loaded at 4 °C on a nickel-nitrilotriacetic acid-agarose affinity resin (Qiagen), and protein fractionation was performed according to the manufacturer's instructions. The fractions containing the CDC2bDN-IC26M fusion protein were pooled.

CDC2bDN-IC26M kinase assays were performed with CDK complexes purified from total plant (*Arabidopsis* seedlings) protein extracts by p13^{suc1}-Sephacryl affinity binding according to Azzi *et al.* (*Eur. J. Biochem.* 203: 353-360). Briefly, p13^{suc1} was purified from an overproducing *E. coli* strain by chromatography in Sephacryl S2000, and conjugated to CNBr-activated Sepharose 4B (Pharmacia) according to the manufacturer's
20 instructions. Total plant protein extracts (300 µg) were incubated with 50 µl 50% (v/v) p13^{suc1}-Sephacryl beads for 2h at 4°C. The washed beads were combined with 30 µl kinase buffer containing ~1 mg/ml CDC2bDN-IC26M, 150 mM ATP and 1 µCi of [³²P]ATP (Amersham). After 20 minutes of incubation at 30°C, samples were analysed by SDS-PAGE and autoradiographed.

25 As shown in Figure 48, the purified CDC2bDN-IC26M protein is phosphorylated by CDKs in vitro.

EXAMPLE 9: PCR AMPLIFICATION OF AtDPb

30 Based on available sequence data of putative plant DP-related partial clones from the databank (soybean DP (AI939068), tomato DP(AW217514), and cotton DP (AI731675)), three oligonucleotides, corresponding to the most conserved part of the DNA-binding and E2F heterodimerization domains (MKVCEKV, SEQ ID NO:240; LNVLMAMD, SEQ ID NO:241 and FNSTPFEL, SEQ ID NO:242), were synthesized and
35 designated A (ATAGAATTCATGAAAGTTTGTGAAAAGGTG, SEQ ID NO:243), B (ATAGAATTCCTGAATGTTCTCATGGCAATGGAT, SEQ ID NO:244) and C (ATAGGATCCCAGCTCAAAAGGAGTGCTATTGAA, SEQ ID NO:245), respectively.

PCR was performed on an Arabidopsis/yeast two-hybrid suspension culture cDNA library. The PCR products were purified, digested with *Eco*RI and *Bam*HI, and ligated into pCR-XL-TOPO vector (Invitrogen). The cloned inserts were sequenced by double-stranded dideoxy sequencing.

5

EXAMPLE 10: CONSTRUCTION OF AtDP and AtE2F MUTANTS, *IN VITRO* TRANSCRIPTION-TRANSLATION SYSTEM AND IMMUNOPRECIPITATION

10 Influenza hemagglutinin (HA)-tagged versions of the wild-type and mutant AtE2Fa and AtE2Fb were constructed by cloning into the pSK plasmid (Stratagene) containing the HA-tag (SEQ ID NO:202). The AtE2F mutants, namely AtE2Fa 1-420 (SEQ ID NO:217), AtE2Fa 162-485 (SEQ ID NO:218), and AtE2Fb 1-385 (SEQ ID NO:206), were obtained by PCR and cloned into the *Eco*RI and *Bam*HI sites of HA-pSK. The *c-myc* (SEQ ID
15 NO:200)-tagged versions of wild-type and AtDP mutants (AtDPa 1-292, SEQ ID NO:114; AtDPa 121-292, SEQ ID NO:211; AtDPa 1-142, SEQ ID NO:208; AtDPa 172-292, SEQ ID NO:213; AtDPa 121-213, SEQ ID NO:212; and AtDPb 1-385, SEQ ID NO:127; AtDPb 182-385, SEQ ID NO:216; AtDPb 1-263, SEQ ID NO:223; AtDPb 1-193, SEQ ID NO:214; and AtDPb 182-263, SEQ ID NO:215) were generated by PCR and cloned
20 into the *Eco*RI and *Pst*I sites of the pBluescript plasmid (Stratagene) containing a double *c-myc* tag. All cloning steps were carried out according to standard procedures, and the reading frames were verified by direct sequencing.

In vitro transcription and translation experiments were performed using the TNT T7-coupled wheat germ extract kit (Promega) primed with appropriate plasmids for 90 min
25 at 30°C. For immunoprecipitation, 10 µl of the total *in vitro* translated extract (50 µl) was diluted at 1:5 in Nonidet P40 buffer (50 mM Tris, pH 7.4, 150 mM NaCl, 1% Nonidet P40, 1 mM phenylmethylsulfonyl fluoride, 10 µg/ml leupeptin/aprotinin/pepstatin) and incubated for 2 h at 4°C with anti-*c-myc* (9E10; BabCo) or anti-HA (16B12; BabCo) antibodies. Protein-A-Sepharose (40 µl 25% (v/v)) was added and incubated for 1 h at 4°C,
30 then the beads were washed four times with Nonidet P40 buffer. Immune complexes were eluted with 10 µl 2 U sodium dodecyl sulfate (SDS) sample buffer and analyzed by 10% or 15% SDS-PAGE and by autoradiography.

An overview of the AtDP and AtE2F fragments and their SEQ ID NOs is given in Table 4.

35

TABLE IV

CCP or partial CCP	SEQ ID NO amino acid sequence	SEQ ID NO DNA sequence
AtE2Fa 226-356	205	228
AtE2Fb 1-385	206	
AtE2Fb 1-127	207	
AtDPa 1-142	208	
AtDPa 42-142	209	
AtDPa 42-292	210	
AtDPa 121-292	211	229
AtDPa 121-213	212	
AtDPa 172-292	213	
AtDPb 1-193	214	
AtDPb 182-263	215	230
AtDPb 182-385	216	231
AtE2Fa 1-420	217	
AtE2Fa 162-485	218	
AtE2Fa 1-38	219	
AtDPa 1-214	220	239
AtDPa 143-292	221	232
AtDPa 143-213	222	233
AtDPb 1-263	223	234
AtE2Fa 232-282	224	235
AtE2Fa 232-352	225	236
AtE2Fb 194-243	226	237
AtE2Fb 194-311	227	238

**EXAMPLE 11: *IN VITRO* INTERACTION BETWEEN AtDPs, AtE2Fs AND
MUTANTS THEREOF ILLUSTRATED BY
IMMUNOPRECIPITATION EXPERIMENTS**

The AtDPa and AtDPb can efficiently interact in vitro with AtE2Fa and AtE2Fb. As a first step in comparing the biochemical properties of AtDPa and AtDPb, the ability of these molecules to heterodimerize with AtE2Fa and AtE2Fb was tested. For this purpose, the coupled in vitro transcription-translation system was used in which the *c-myc*-tagged AtDPa or AtDPb was co-expressed with the HA-tagged AtE2Fa or AtE2Fb. One part of each sample was resolved by SDS-PAGE (Figures 50 and 51, panels A), while another part was subjected to immunoprecipitation with monoclonal anti-*c-myc* antibodies (Figures 50 and 51, panels B). In the absence of DP proteins, no AtE2F2a or AtE2F2b was precipitated by the anti-*c-myc* antibodies (Figure 51, panel B, lane 1). However, both HA-

AtE2F proteins co-precipitated reproducibly with *c-myc*-tagged AtDPa (Figure 50, panel B, lanes 1 and 2) and AtDPb (Figure 51, panel B, lanes 3 and 4). Identical results were obtained in a reciprocal experiment with anti-HA monoclonal antibodies. These data revealed that both Arabidopsis DP-related proteins interacted *in vitro* with the different Arabidopsis E2F-related proteins.

The conserved dimerization domain of the AtE2Fs seemed to be important for the interaction with the AtDPs, because mutational analysis showed that deletion neither of the N-terminal extension nor the C-terminal part of AtE2Fa and AtE2Fb impaired the interaction with the DP (Figures 50 and 51, panels B). Similar results were obtained by two-hybrid analysis (see Table 5 of Example 12). To test whether the structural requirements for heterodimerization of the AtDPs were similar to those of their animal homologs, several deletion mutants of AtDPa and AtDPb were constructed (for a schematic illustration, see Figures 52 and 53), tagged with the *c-myc* epitope (Figures 54 and 55, panels A). The interactions between the mutant AtDPs and AtE2Fb were analyzed in immunoprecipitation experiments with the specific anti-HA or anti-*c-myc* antibodies (Figures A6 and A7, panels B and C, respectively). As shown in Figures 54 and 55, mutant AtDP proteins with deleted DNA-binding domain could bind sufficiently to the co-translated HA-AtE2Fb proteins (Figure 54, panel C, lane 2; and Figure 55, panel C, lane 2). No detectable interaction was found between the AtE2Fb protein and mutant DP proteins containing the complete DNA-binding domain, but lacking the putative dimerization domain (Figure 54, panel C, lane 3; Figure 55, panel C, lane 4). Thus, the N-terminal part of both AtDP proteins, including the conserved DNA-binding domain, was not sufficient for the *in vitro* interaction to occur. In contrast, a mutant form of AtDPb (amino acids 1-263; SEQ ID NO:223) could bind to AtE2Fb (Figure 55, panel C, lane 3), indicating that the region of AtDPb between amino acids 182 and 263 was required for interaction with AtE2Fb.

To confirm this hypothesis, a deletion mutant of AtDPb (182-263, SEQ ID NO:215) was constructed and, as expected, it could bind to AtE2Fb (Figure 56). The requirement for the homologous dimerization domain of AtDPa for the interaction with AtE2Fb was supported by a binding assay in which the mutant AtDPa 172-292 (SEQ ID NO:213), with the N-terminal part of the dimerization domain deleted, failed to bind to AtE2Fb (Figure 54, panels B and C, lanes 4). However, when the E2F-binding activity of the predicted dimerization domain of the AtDPa (amino acid positions 121-213, SEQ ID NO:212) was tested, no interaction could be detected between this region and the AtE2Fb protein (Figure 54, panel B, lane 5). These data indicate that other carboxyl-terminal regions of AtDPa are required for the stable interaction with AtE2Fb.

EXAMPLE 12: YEAST TWO-HYBRID EXPERIMENTS FOR SHOWING INTERACTION BETWEEN DP AND E2F MUTANTS

For library screening, vectors and strains (HF7c) were provided with the
 5 Matchmaker two-hybrid system (Clontech). The dimerization and DNA-binding domains of the AtE2Fa (amino acids 226-356; SEQ ID NO:205) were amplified by polymerase chain reaction (PCR) and subcloned in-frame with the GAL4 DNA-binding domain of pGBT9 (Clontech) to create the bait plasmid pGBTE2Fa226-356. Screens were performed as described previously (De Veylder et al. 1999; Planta 208, 453-462). A second library
 10 screening was performed with the AtE2Fb construct (pGBTE2Fb-Rb) lacking the Rb-binding domain (amino acids 1-385; SEQ ID NO:206). Plasmids from interacting clones were isolated and sequenced.

For the yeast two-hybrid interaction experiments, a number of yeast two-hybrid prey (in pAD-GAL424) plasmids were created by PCR amplification of fragments from
 15 the AtDPa (DPa 1-292, SEQ ID NO:114; DPa 1-142, SEQ ID NO:208; DPa 42-142, SEQ ID NO:209; DPa 42-292, SEQ ID NO:210; DPa 121-292, SEQ ID NO:211; DPa 121-213, SEQ ID NO:212; and DPa 172-292, SEQ ID NO:213) and AtDPb (DPb 1-385, SEQ ID NO:127; DPb 1-193, SEQ ID NO:214; DPb 182-263, SEQ ID NO:215; and DPb 182-385, SEQ ID NO:216) genes and confirmed by sequencing. Different combinations between
 20 bait (pGBTE2Fa226-356, pGBTE2Fb-Rb, or pGBTE2Fb 1-127, SEQ ID NO:207) and prey constructs were transformed into yeast cells and assayed for their ability to grow on His⁻ minimal media after 3 days of incubation at 30°C. Bait plasmids co-transformed with empty pAD-GAL424 and prey plasmids co-transformed with empty pGBT9 were assessed along as controls for the specificity of the interaction.

25 An overview of the AtDP and AtE2F fragments and their SEQ ID NOs is given in Table 4.

The results obtained were confirmed by two-hybrid interaction analysis. pGBTE2Fa226-356 and pGBTE2Fb-Rb were co-transformed in an appropriate yeast reporter strain with a plasmid producing the full-length AtDPa or AtDPb protein fused to
 30 the GAL4 transactivation domain. The specific reconstitution of GAL4-dependent gene expression measured as the ability to grow in the absence of histidine confirms the interaction between the two DP and E2F proteins (Table 5).

TABLE V
AtDPs and AtE2Fs interaction in yeast two-hybrid assays.

Baits	Preys												
	DPa 1-292	DPa 1-142	DPa 42-142	DPa 42-292	DPa 121-292	DPa 121-213	DPa 172-292	DPb 1-385	DPb 1-193	DPb 182-263	DPb 182-385	E2Fa 226-356	pAD- GAL424
pGBT E2Fa 226-356	+	-	-	+	+	-	-	+	-	+	+	-	-
pGBT E2Fb-Rb	+	-	-	+	+	-	-	+	-	+	+	-	-
pGBT E2Fb 1-127	-	NT	NT	NT	NT	NT	NT	-	NT	NT	NT	-	-
pGBT DPa 1-292	-	NT	NT	NT	NT	NT	NT	-	NT	NT	NT	+	-
pGBT DPb 1-385	NT	NT	NT	NT	NT	NT	NT	-	NT	NT	NT	+	-
pGBT9	-	-	-	-	-	-	-	-	-	-	-	-	-

Different combinations between AtE2Fs bait and AtDPs prey constructs were tested for growth on His⁺ minimal media.

-, no interaction; +, positive interaction; NT, not tested.

EXAMPLE 13: RNA ISOLATION AND REVERSE TRANSCRIPTION-(RT)-PCR ANALYSIS OF AtDP And AtE2F EXPRESSION

A. thaliana (L.) Heynh. cell suspension cultures were maintained as described previously (Glab et al. 1994, FEBS Lett. 17, 207-211). The cells were partially synchronized by the consecutive addition of aphidicolin (5 µg/ml) and propyzamide (1.54 µg/ml). The aphidicolin block was left for 24 hours. The cells were washed for 1 hour in B5 medium before the addition of propyzamide. Samples were taken at the end of the 24 hour aphidicolin block, at the end of a 1 hour washing step, and at 1, 2, 3, and 4 hours after the addition of propyzamide to the culture medium. Total RNA was isolated from the Arabidopsis cell suspension culture according to Magyar et al. (1997), Plant Cell 9, 223-235, and with the Triazol reagent (Gibco/BRL) from different organs. Semi-quantitative RT-PCR amplification was carried out on reverse-transcribed mRNA, ensuring that the amount of amplified product stayed in linear proportion to the initial template present in the reaction. 10 µl from the PCR was transferred onto Hybond-N/ membrane, hybridized to fluorescein-labeled gene-specific probes (Gene-Images random prime labeling module; Amersham Pharmacia Bio-tech), detected with the CDP-Star detection module (Amersham), and visualized by short exposure to Kodak X-OMAT autoradiography film.

The following primer pairs (forward and reverse) were used for the amplification:

5' -ATAGAATTCATGTCCGGTGTCTGACGA-3' (SEQ ID NO:249, *Eco*RI site underlined) and 5' -ATAGGATCCCACCTCCAATGTTTCTGCAGC-3' (SEQ ID NO:250, *Bam*HI site underlined) for AtE2Fa (GenBank accession number AJ294533);

5' -ATAGAATTCGAGAAGAAAGGGCAAT CAAGA-3' (SEQ ID NO:251, *Eco*RI site underlined) and 5' -ATACTGCAGAGAAATCTCGATTTCGACTAC-3' (SEQ ID NO:252, *Pst*I site underlined) for AtDPa (GenBank accession number AJ294531);

5' -GCCACTCTCATAGGGTTCTC CATCG-3' (SEQ ID NO:253) and 5' -GGCATGCCTCCAAGATCCTTGAAGT-3' (SEQ ID NO:254) for Arath;CDKA;1 (Genbank accession number X57839); 5' -GGGTCTTGGTCGTTTTACTGTT-3' (SEQ ID NO:255) and 5' -CCAAGACGATGACAACAGATACAGC-3' (SEQ ID NO:256) for Arath;CDKB1;1 (Genbank accession number X57840);

5' -ATAAACTAAATCTTCGCTGAA- 3' (SEQ ID NO:257) and 5' -CAAACGCGGATCTGAAAACT-3' (SEQ ID NO:258) for histone H4 (Genbank accession number M17132); 5' -TCTCTCTTCCAAATCTCC-3' (SEQ ID NO:259) and 5' -AAGTCTCT CACTTTCTCACT-3' (SEQ ID NO:260) for ROC5 (AtCYP1, GenBank accession number U072676) (Chou and Gasser 1997, Plant Mol. Biol. 35, 873-892);

5' -CTAAGCTCTCAAGATCAAAGGCTTA-3' (SEQ ID NO:261) and 5' -TTAACATTGCAAAGAGTTTCAAGGT-3' (SEQ ID NO:262) for actin 2 gene (GenBank accession number U41998) (An et al. 1996, Plant J. 10, 107-121).

**EXAMPLE 14: THE AtDPa And The AtE2Fa GENES ARE CO-EXPRESSED
IN A CELL CYCLE PHASE-DEPENDENT MANNER**

The identification of the AtDPa in a yeast two-hybrid screen as a gene encoding an
5 AtE2Fa-associating protein indicated that it might act cooperatively in the plant cells as a
functional heterodimer. To strengthen this hypothesis, we investigated whether both genes
were co-regulated at the transcriptional level. Tissue-specific expression analysis revealed
that both genes were clearly up-regulated in flowers and were very strongly transcribed in
actively dividing cell suspension cultures (Figure 57). Expression in these tissues could be
10 a sign for the correlation between the actual proliferation activity of a given tissue and the
transcript accumulation, as can be seen from the *Arath*;CDKB1;1 gene. AtDPa transcripts
were also detectable in leaf and, to a lesser extent, in root and stem tissues, whereas
AtE2Fa transcripts were virtually undetectable in roots and stem with only slight levels of
expression in leaf tissues. Cell cycle phase-dependent gene transcription was studied using
15 an Arabidopsis cell suspension that was partially synchronized by the sequential treatment
with aphidicolin and propyzamide. The Arabidopsis histone H4 and the *Arath*;CDKB1;1
gene were included to monitor the cell cycle progression (Figure 58) (Chaubet et al. 1996,
Plant J. 10, 425-435; Segers et al. 1996, *Plant J.* 10, 601-612). Bearing in mind the partial
synchronization of the culture, it can be observed that histone H4 transcript levels peaked
20 immediately after the removal of the inhibitor and decrease gradually thereafter (Figure
58). The opposite expression pattern could be observed for the *Arath*;CDKB1;1 gene,
illustrating that cells entered the G2-M phases with partial synchrony. Within this
experimental setting, the AtDPa and the AtE2Fa genes show a very similar expression
pattern. Both exhibit higher transcript accumulation before the peak of histone H4 gene
25 expression and quickly decay in the following samples (Figure 58). The similarity in the
expression patterns of Arabidopsis AtDPa and AtE2Fa supports the possibility that they act
cooperatively as a heterodimer during the S phase.

**EXAMPLE 15: TRANSFORMATION OF ARABIDOPSIS THALIANA WITH
30 CaMV35S::DPa**

Arabidopsis plants were transformed (using the in planta flower dip method; Clough
and Bent, *Plant J.* 16:735-743, 1998) with a construct containing the DPa gene under the
control of the *CaMV 35S* promoter. The lines were molecularly analysed by northern
35 blotting. As can be seen in Figure 59, all lines showed increased DPa levels in comparison
with the untransformed control. Generally, two classes of lines were observed: weakly
expressing (e.g., 16) and strongly expressing (e.g., 23) lines (see Figure 59). The plants are
subsequently analyzed for phenotypic alterations as described herein.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than
5 routine experimentation, many equivalents to the specific embodiments of the invention
described herein. Such equivalents are intended to be encompassed by the following
claims.

What is claimed:

1. An isolated nucleic acid molecule selected from the group consisting of:
 - 5 (a) a nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NOs:3, 6, 12, 13, 29, 41, 42, or 45.
2. An isolated nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111.
- 10 3. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence set forth in SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111.
- 15 4. An isolated nucleic acid molecule selected from the group consisting of:
 - a) a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to the nucleotide sequence of SEQ ID NOs:3, 6, 12, 13, 29, 41, 42, or 45, or a complement thereof;
 - 20 b) a nucleic acid molecule comprising a fragment of at least 50 nucleotides of a nucleic acid comprising the nucleotide sequence of SEQ ID NOs:3, 6, 12, 13, 29, 41, 42, or 45, or a complement thereof;
 - c) a nucleic acid molecule which encodes a polypeptide comprising an amino acid sequence at least about 60% identical to the amino acid sequence of SEQ ID
 - 25 NOs:69, 72, 78, 79, 95, 108, or 111; and
 - d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111, wherein the fragment comprises at least 15 contiguous amino acid residues of the amino acid sequence of SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111.
- 30 5. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1, 2, 3, or 4 under stringent conditions.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which
- 35 is complementary to the nucleotide sequence of the nucleic acid molecule of any one of claims 1, 2, 3, or 4.

7. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1, 2, 3, 4, or 5, and a nucleotide sequence encoding a heterologous polypeptide.
- 5 8. A vector comprising the nucleic acid molecule of any one of claims 1, 2, 3, or 4.
9. A cell comprising the nucleic acid molecule of any one of claims 1, 2, 3, or 4.
- 10 10. A host cell transfected with the vector of claim 8.
11. A method of producing a polypeptide comprising culturing the host cell of claim 10 in an appropriate culture medium to, thereby, produce the polypeptide.
- 15 12. An isolated polypeptide selected from the group consisting of:
- a) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111;
 - 20 b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of SEQ ID NOs:3, 6, 12, 13, 29, 41, 42, or 45 under stringent
 - 25 conditions;
 - c) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 60 % identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NOs:3, 6, 12, 13, 29, 41, 42, or 45;
 - d) a polypeptide comprising an amino acid sequence which is at least
 - 30 60% identical to the amino acid sequence of SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111.
13. The isolated polypeptide of claim 12 comprising the amino acid sequence of SEQ ID NOs:69, 72, 78, 79, 95, 108, or 111.
- 35 14. The polypeptide of claim 12, further comprising heterologous amino acid sequences.
15. An antibody which selectively binds to a polypeptide of claim 12.

16. A method for detecting the presence of a polypeptide of claim 12 in a sample comprising:

- 5 a) contacting the sample with a compound which selectively binds to the polypeptide; and
- b) determining whether the compound binds to the polypeptide in the sample to thereby detect the presence of a polypeptide of claim 12 in the sample.

17. The method of claim 16, wherein the compound which binds to the polypeptide is an antibody.

18. A kit comprising a compound which selectively binds to a polypeptide of claim 12 and instructions for use.

19. A method for detecting the presence of a nucleic acid molecule of any one of claims 1, 2, 3, or 4 in a sample comprising:

- a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and
- b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample to thereby detect the presence of a nucleic acid molecule of any one of claims 1, 2, 3, or 4 in the sample.

20. The method of claim 19, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

21. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of any one of claims 1, 2, 3, or 4 and instructions for use.

22. A method for identifying a compound which binds to a polypeptide of claim 12 comprising:

- a) contacting the polypeptide, or a cell expressing the polypeptide with a test compound; and
- b) determining whether the polypeptide binds to the test compound.

23. The method of claim 22, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) detection of binding by direct detection of test compound/polypeptide binding;
- 5 b) detection of binding using a competition binding assay; and
- c) detection of binding using an assay for CCP activity.

24. A method for modulating the activity of a polypeptide of claim 12 comprising contacting the polypeptide or a cell expressing the polypeptide with a
10 compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

25. A method for identifying a compound which modulates the activity of a polypeptide of claim 12 comprising:
15 a) contacting a polypeptide of claim 12 with a test compound; and
 b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

20 26. A transgenic plant comprising the nucleic acid molecule of any one of claims 1, 2, 3, or 4.

27. The transgenic plant of claim 26, wherein the plant is a monocot plant.

25 28. The transgenic plant of claim 26, wherein the plant is a dicot plant.

29. The transgenic plant of claim 26, wherein the plant is selected from the group consisting of arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower, and canola.

30

30. A method for modulating the growth of a plant, comprising introducing into the plant a CCP modulator in an amount sufficient to modulate the growth of the plant, thereby modulating the growth of the plant.

35 31. The method of claim 30, wherein the CCP modulator is a small molecule.

32. The method of claim 30, wherein the CCP modulator is capable of modulating CCP polypeptide activity.

33. The method of claim 32, wherein the CCP modulator is an anti-CCP antibody.

5 34. The method of claim 32, wherein the CCP modulator is a CCP polypeptide comprising the amino acid sequence of SEQ ID NOs: 67-132, 205, 211, 215-216 or 220-227, or a fragment thereof.

35. The method of claim 30, wherein the CCP modulator is capable of
10 modulating CCP nucleic acid expression.

36. The method of claim 35, wherein the CCP modulator is an antisense CCP nucleic acid molecule.

15 37. The method of claim 35, wherein the CCP modulator is a ribozyme.

38. The method of claim 35, wherein the CCP modulator comprises the nucleotide sequence of SEQ ID NOs: 1-66 or 228-239, or a fragment thereof.

20 39. The method of claim 30, wherein the plant is a monocot plant.

40. The method of claim 30, wherein the plant is a dicot plant.

41. The method of claim 30, wherein the plant is selected from the group
25 consisting of arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower, and canola.

42. A method for modulating the cell cycle in a plant, comprising introducing
into the plant a CCP modulator in an amount sufficient to modulate the cell cycle in the
30 plant, thereby modulating the cell cycle in the plant.

43. The method of claim 42, wherein the plant is a monocot plant.

44. The method of claim 42, wherein the plant is a dicot plant.

35

45. The method of claim 42, wherein the plant is selected from the group consisting of arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower, and canola.

1/65

A.**CCP molecule: CCP1 nucleotide sequence (CDC2bDN-IC19):**

cttttaagttgggggatgttttcgattttgaaatttgatttcttcaagagaagagatttaataatgaaa
 ataaataacttccgcagataacgaagaagaagaaaatggttagatcagatgaaaatagccttgga
 ttaatcgatcaatgagtcctcaaggtaccctaaatcgatcgattttgttattaaaaatcaaaac
 tttcgttctctttgatttttccccaaattgattttgaatttacttgatgtagggggaggagtag
 taggaaagatcaagacgacggaacaacaggaccgacaagaagagcactaagtactattaacaag
 aacatcactgaagcgccgtcttacccttatgctgtcaacaagagatcagtttctgaaagagatgg
 catttgtaataaaaccacctgtgcatcgaccagttacttaggaagtttgctgctcagttagcagatc
 ataagccacatatccgtgatgaggaaactaagaaaccagactcagtttcaagtgaagaaccagag
 acgattatcattgatgtggatgaaagtgaataagaaggaggtgactctaataagccaatgtttgt
 acaacatactgaagcaatgctggaggagattgaacagatggagaaggagattgaaatggaagatg
 cagacaaagaagaagagcctgtgatcgatattgatgcctgtgataagaataatcctttggctgcg
 gttgaatatatccatgatatgcataccttctacaagaattttgagaaacttagttgcgtgcctcc
 taactataatggacaatcaacaagatcttaatagagagaatgagaggaatcctcattgactggtaa
 ttgaggtgactacaagtttgaactgatggaggaaactctttatctcacaatcaatgtcatcgac
 agattccttgcggttcatcaaatcgtgaggaaaaagcttcagcttggttggtggttactgctttgtt
 gcttgcatgtaaatatgaagaagtttcagttccagtggttagatgatctcatcttgatctctgaca
 aagcttactctagaagagaagtgctagatatggagaagctaataggccaacaccttgcaattcaat
 ttctctctaccaactccatatgttttcatgaaacgatttctcaaagctgccaatctgacaagaa
 gcttgagattttatcattctttatgatcgagctttgccttggtgagtagatgagatgctagagtatc
 ttcatctaaagctggcgccctcagcaatctacactgctcagtggtacacttaagggtttgaagaa
 tggagcaaaacctgtgagtttcacacaggctacaacgaaaaacagctactggcatgtgagagaaa
 gatggttgctttccatcacaaggcaggaaacagggaagctcacaggagttcacagaaagtacaaca
 catctaagttctgtcatgctgcaagaactgaaccagctgggtttctgattcaatattaataagaa
 tctaataatgacttaactcgagtttttctttagaacaaaaagagtgtagagagaagagagatagta
 gagcaagttgccccaaatgggagaagaatggatcttttagatatcatggcaagtagccccaaaaga
 gtgtattcttctcttttctaaggtcttttagatctttcttcacttgagagagaataaaaagaatctt
 ctgaaaaaaaaaaaaaaaaaaaaaaaaa

B.**CCP molecule: CCP1 amino acid sequence (CDC2bDN-IC19):**

MVRSDENSLGLIGMSLQGTLNRSILLKIKTFVLFDFSPKLIILNLLDVGGGVVGKIKTTATTGP
 TRRALSTINKNITEAPSPYAVNKRVSERDGINCKPPVHRPVTRKFAAQLADHKPHIRDEETKK
 PDSVSSEEPETIIIDVDESDEGGDSNEPMFVQHTTEAMLEEIEQMEKEIEMEDADKEEPPVIDID
 ACDKNNPLAAVEYIHDMTFYKNFEKLSVPPNYMDNQDLNERMRGILIDWLEIYVHYKFELMEE
 TLYLTINVIDRFLAVHQIVRKKLQLVGVTALLLACKYEEVSVPVDDLLILISDKAYSRRREVLDMEE
 KLMANTLQFNFSLPYPYFMKRFLKAAQSDKKLEILSFFMIELCLVEYEMLEYLPSKLAASAIYT
 AQCTLKGFEESKTCFHTGYNEKQLLACARKMVAFHKKAGTGKLTGVHRKYNTSKFCHAARTEP
 AGFLI

FIGURE 1

2/65

CCP molecule: CCP2 nucleotide sequence (CDC2bDN-IC20):

aaccacggtcaattctttttcaaaggcatatatctctctgtttcaaactttgtgtctcttcttc
tccttctctgatcggttcgttttctggacgagagagatggttaaatccgggtcaagggaaggagccc
gattcgggtactgctgctggtgggtcaaactccgacccgtttcctgcgaatcttcgagttcttgt
cgttgatgatgatccaacttgtctcatgatcttagagaggatgcttatgacttgtctctacagag
taactaaatgtaacagagcagagagcgcatgtctctgcttcggaagaacaagaatggttttgat
attgtcattagtgtgtcatatgcctgacatggatggtttcaagctccttgaacacggttgggtt
agagatggatttacctgttatcatgatgtctgcggatgattcgaagagcggttgtgttgaaaggag
tgactcacgggtgcagttgattacctcatcaaacgggtacgtattgaggctttgaagaatatatgg
caacatgtggtgcggaagaagcgtaac-gagtggaaatgtttctgaacattctggaggaagtattg
in CDC2bDN-IC20:c g
aagatactggcgggtgacaggacaggcagcagcagcatagggaggatgctgataacaactcgtct
tcagttaatgaagggaacgggaggagctcgaggaagcggaagggaagaggaagtagatgatcaagg
ggatgataaaggagactcatcgagtttaagaaacacgcgtgggttgggtctgttgattgcac
agcagtttgttgcgtgtgtaacagctaggcgttgacaaagctgttcctaagaagatcttagag
atgatgaatgtaccgggctaacgcgagaaaaacgtagccagtcacctccagaagtatcggatata
tctgagacggccttgaggagtatcgcaacaccaaggaaatatgaaccattcgtttatgactggtc
aagatcagagttttggacctctttcttcgttgaaatggattttgatcttcaatctttagctgttact
ggtcagctccctcctcagagccttgacagcttcaagcagctggtcttggccggcctacactcgc
taaaccagggatgtcggtttctccccttgtagatcagagaagcatcttcaactttgaaaacccaa
aaataagatttgagacggacatggtcagacgatgaacaatggaaatttgcttcatggtgtccca
acgggtagtacatgcgtctgcgtcctggacagaatgttcagagcagcggaatgatgttgccagt
agcagaccagctacctcgaggaggaccatcgatgctaccatccctcgggcaacagccgatattgt
caagcagcggtttcaagaagaagcgatctcactggtgcgctggcggttagaaacagtatccccgag
accaacagcagagtgttaccaactactcactcggtcttcaataacttcccccgggatctacctcg
cagcagcttcccgttggcaagtgtcccagggtttcagttccagtatcagtttcttaccagaag
aggtcaacagctcggtatgcaaaaggaggttcatcagctgctactgctggatttggttaaccaagc
tacgacataatttaacgattttccgcagcaccaacagcacaacaagaacatcagcaataaactaaa
cgattgggatctgcggaatatgggattgggtcttcagttccaatcaggacgcagcaactgcaaccg
caaccgcagcattttccacttcggaagcatactcttcgtcttctacgcagagaaaaagacgggaa
acggacgcaacagttgtgggtgagcatgggcagaacctgcagtcaccgagccggaatctgtatca
tctgaaccacgttttatggacgggtggttcagtcagagtgaagtcaagaagatctgatgagcgca
tttctcaaacaggaaggcatcccatccgtagataacgagttcgaatttgacggatactccatcga
taataatccagggtctgactacagaaaactcagactagactgcaagattctttgttttcttctccct
ccttcgaggtacaaagctcaaaacatggcaataaccgaagggaagataga

FIGURE 2

3/65

CCP molecule: CCP2 amino acid sequence (CDC2bDN-IC20):

MVNPGHGRGPDSGTAAGGSNSDPFPANLRVLVVDDDPTCLMILERMLMTCLYRVTKCNRAESALS
LLRKNKNGFDIVISDVHMPDMDGFKLLEHVGLEMDLPVIMMSADDSKSVVLKGVTHGAVDYLIKP
VRIEALKNIWQHVVRKKRNEWNVSEHSGGSIEDTGGDRDRQQQHREDADNNSSSVNEGNRSSRK
RKEEEVDDQGDDKEDSSSLKKPRVVWSVELHQQFVAAVNQLGVDKAVPKKILEMMNVPGLTRENV
ASHLQKYRIYLRRLGGSQHQGNMNHSFMTGQDQSFGPLSSLNGFDLQSLAVTGQLPPQSLAQLQ
AAGLGRPTLAKPGMSVSPLVDQRSIFNFENPKIRFGDGHGQTMNNGNLLHGVPTGSHMRLRPGQN
VQSSGMMLPVADQLPRGGPSMLPSLGQQPILSSSVSRSDLTGALAVRNSIPETNSRVLPTTHSV
FNNFPADLPRSSFPLASAPGISVPVSVSYQEEVNSSDAKGGSSAATAGFGNPSYDIFNDFPQHQQ
HNKNISNKLNDWDLRNMGLVFSSNQDAATATATAAFSTSEAYSSSTQRKRRETDATVVGEHGQN
LQSPSRNLYHLNHVFMDGGSVRVKSERVAETVTCPPANTLFHEQYNQEDLMSAFLKQEGIPSVDN
EFEFDGYSIDNIQV

FIGURE 3

4/65

A.

CCP molecule: CCP3 nucleotide sequence (CDC2bDN-IC21):

aggctgtgttttatcgtgggattttttaaacatg~~gggaaggaaaatgctgtg~~tctcgccattcac
 tcgttcccttgccctctgctttgcgcgcttcagaagtgacttctactacacagaatcaacagagag
 taaacacaaaaagaccagccttgaggatacaagagccactggacccaacaagaggaagaagcga
 gcggttctaggggagatcacaaatgttaactccaatacagctatacttgaggccaaaaacagcaa
 gcagataaagaaaggacgcggtcatggattggcgagtacatcccagttggcaacttctgttactt
 cagaagtcacagatcttcagtcaggaccgatgcaaaagttgaagttgcatcaaatacagcagga
 aacctttctgtttctaaaggcacagataacacagctgataactgtattgagatatggaattctag
 attgcctccaagacctcttgaggatcagcttctacagctgagaaaagtgtgttattggttagtt
 caactgtaccggatatcccaaaatttgtagacatcgattcagatgacaaggatccctttactgtgc
 tgcttctatgccctgaaatccactacaatttgctgtttcagagcttaaacgcagaccacttcc
 ggactttatggagagaatacagaaggatgtcaccagtcctatgcggggaattctggttgattggc
 ttgtggaggtctctgaagaatacacacttgcattctgacactctctacctcacagtgtatctcata
 gactgggttcctccatggaaactacgtgcaaagacagcaacttcaactgctcggcatcacttgcat
 gctaattgcctcgaagtatgaggaaatctctgctccacgcattgaggagttttgcttcattacgg
 ataacacctacacaagagatcaggtcctggaaatggagaaccaagtaacttaagcatttttagcttt
 caaatatacactccactccaaaacggttccttaggagatttctcagagcagctcaagcctctcg
 cctgagcccaagccttgaagtcgagtttctagccagctatctaacagagttgacattaatagact
 accatttcttaaagtttcttccctccgttggttgctgcttcagcggtttttctcgccaagtggaca
 g (in CDC2bDN-IC21)
 atggaccaatcaaaccacccatggaatccaacacttgagcattacacaacgtacaaagcatcgga
 tctgaaagcatctgttcatgccttacaagatctgcagcttaacaccaaaaggttgcccttgagcg
 ctatagcatgaagtataggcaagagaaatacaaatctgtggcggttctcacgtctccaaagcta
 ttgacacgctattctgaagggtttcaactcctaaccgataatagtttt

B.

CCP molecule: CCP3 amino acid sequence (CDC2bDN-IC21):

MGKENAVSRPFTRSLASALRASEVTSTTONQQRVNTKRPALEDTRATGPNKRKKRAVLGEITNVN
 SNTAILEAKNSKQIKKGRGHGLASTSQLATSVTSEVTDLQSRDPAKVEVASNTAGNLSVSKGTDN
 TADNCIEIWNRLPPRPLGRSASTAEKSAVIGSSSTVPDIPKFVDIDSDDKDPLLCCLYAPEIHYN
 LRVSELKRRLPDFMERIQKDVTQSMRGILVDWLVEVSEEYTLASDTLYLTVYLIWFLHGNVQ
 RQQLQLLGITCMLIASKYEEISAPRIEEFCFITDNTYTRDQVLEMENQVLKHFSFQIYTPTPKTF
 LRRFLRAAQASRLSPSLEVEFLASYLTETLIDYHFLKFLPSVVAASAVFLAKWTMDQSNHPWNP
 TLEHYTTYKASDLKASVHALQDLQNLTKGCPLSAIRMKYRQEKYKSVAVLTSPKLLDTLF

FIGURE 4

6/65

A.

CCP molecule: CCP5 nucleotide sequence (CDC2bDN-IC39):

ggcacgagaaaaaaaatggttaactcatgcgagaacaaaaatcttcgttaaaccacttcaacga
cgattcttcaagatgaaacaagaagtagaaaattcggacaagagatgaagagggagaagagaaga
gtgttgcggtgtgattaaccagaatctcgctgggtgcaagagtttatccttgtgtgtcaacaagaa
aggaagcttattgtctaataagcaagaagaagaagaaggatgtcaaaagaagaagtttgattcctt
tgcgtccttcagttacaagatctggagttgaggaagagactaacaagaagctgaagccctcagtt
ccaagtgcataacgacttcgggtgattgtatatatttattgatgaggaggaagctacattggaccttcc
aatgccaatgtcgcttgagaaaccatacattgaagctgatccaatggaagaagttgagatggagg
atgtaacagtggaagaaccgatcggtgatattcgatgtcttagactcgaagaactcgcttgcggct
gttgaatatgttcaagatctttacgcatttttacagaacaatggagagatttagttgtgttccagt
agactatatgatgcaacaaatcgacttaaacgagaagatgagagcaataactaactcgactggttaa
tcgagggtacatgacaagtttgatctgatgaacgagacactgtttctgacagtgaatctgatagat
agattcttgtccaagcaaaatgttatgagaaagaagcttcagcttgtagggtagtagctttgct
gttagcttgttaagtatgaggaggtttcggttcctgttgcgaagatttagtactcatttcggaca
aagcgtatacaggaacgatgttctagagatggagaaaacaatgttgagtactttgcaattcaat
atctcgttaccgacacaataaccggttcttgaaaagattcctcaaggcagctcaagcagacaagaa
gtgtgaggtcttggcgtcggttcttgatcgagcttgcccttgtggagtacgagatgcttcggtttc
caccatcattactagctgccacatctgtgtacactgctcaatgtacacttgatgggtccaggaaa
tggaacagttacatgtgaattccattgtcattactctgaagaccagctcatggaatgttcacggaa
gctggtgagttctgcatcagagggcggtgcagagaaacttaacaggagtatataggaagtacagca
caagcaaattttggttacatagcaaaatgtgaagctgcacactttctagtgtctgaggtctcatcat
tcttaataccaaaggaacagtagtaagtagtttgtagagcttcctgacatagttccctcattcact
ctgtagcacaataagaagaaacaaaaaaagccaattaaatttgtcttatgattgattctgt
ttttttgttgttactctttgttcacttcacttgcagtattaaactctacaatgaatgataaatg
attgaatcatttcattctttgttcagaatgaaatgtattttgtatcttatttgagctaaaaaaa
aaaaaaaaaaaaaactcgaggggggccccggtaccc

B.

CCP molecule: CCP5 amino acid sequence (CDC2bDN-IC39):

MVNSCENKIFVKPTSTTILQDETRSRKFGQEMKREKRVLRVINQNLGARVYPCVVNKKGSLLS
NKQEEEEGCQKKKFDSLRLPSVTRSGVEEETNKKLKPSVPSANDFGDCIFIDEEATLDLPMPSL
EKPYIEADPMEEVEMEDVTVEEPIVDIDVLD SKNSLA AVEYVQDL YAFYRTMERFSCVPVDYMMQ
QIDLNEKMRATLIDWLVIEVHDKFDLMNETLFLT VNLIDRFLSKQNV MRKKLQLVGLVALLLACKY
EEVSVPVVEDLVLISDKAYTRNDVLEMEKTM LSTLQFNISLPTQYPFLKRFLKAAQADKKCEVLA
SFLIELALVEYEMLRFP PSLAATS VYTAQCTLDGSRKWNSTCEFHCHYSEDQLMECSRKL VSLH
QRAATGNLTGVYRKYSTSKFGYIAKCEAAHFLVSESHHS

FIGURE 6

5/65

A.

CCP molecule: CCP4 nucleotide sequence (CDC2bDN-IC26M):

atggggaagaagtgtgatttatgtaacggtggtgcaagaatgtattgcgagtcagatcaagctag
tttatggtgggattgacggttaaagttcacggcgctaatttcttggtagctaaacacacgcggtt
gtcttctctgtagcgcttgtcagtcctttacgccgtggaaagctactgggcttcgtcttggccca
actttctccgtctgacgagtcattgcgtcgctcttaaaaacgcccggcggtggccgtggaaacagagt
tttatcggagaatcggtggtcaggaggaggttaatatgtttcgagtcggaagaagatcggtattagag
aagatcacggtgacggtgacgacgaggagtcttacgatgatgatgaggaagaagatgaggatgaa
gagtacagcgacgatgaggatgaggatgatgatgaggatggtgatgatgaggaagcgggagaatca
agttgtgccgtggtctgcggcgccgcaagttcctccggtgatgagttcttcatcttctgacggag
gaagcggaggttcagtgacgaagaggacgagggctagagagaattcagatcttctctgctccgat
gatgagatcggaagctcttcagctcaagggtcaaactattctcgccggttgaaagcgatcggcggtt
taaatacaacggttggtgtttaactcacaactctaccgtatcgtcagaatgaacggcgccgatacat
cgtcttctccgatctttgcatctccaaaacaagaagagatctcagccggttgattcc

B.

CCP molecule: CCP4 amino acid sequence (CDC2bDN-IC26M):

MGKKCDLCNGVARMYCESDQASLCWDCDGKVHGANFLVAKHTRCLLC SACQSLTPWKATGLRLGP
TFSVCESCVALKNAGGGRGNRVLS ENRGQEEVNS FESEEDRIREDHGDGDDAESYDDDEEEDDE
EYSDDEDEDDEDGDDEEAENQVVPWSAAAQVPPVMSSSSSDGSGGGSVTKRTRARENSDLLCSD
DEIGSSSAQGSNYSRPLKRSAFKSTVVV

FIGURE 5

7/65

CCP molecule: CCP6 nucleotide sequence (CDC2bDN-IC57):

atttgagaggaagctttattttgtgtgttagatggggaataatcctccgcagtccttctggtacccagggtca
 gcattttgttcctgcagcttcacaaccttttcaccttatggacatgtacctccaaatgttcaaagtcagc
 ctccacagtagttctcagccgatacagcagcagcagctctttccagtgcagaccagggtcagcctgtgcatact
 acatcatcctcacaggctgtatcagttccgtatattcaaacgaacaagattctcacttctggatctactca
 accacagccaaatgcacctccaatgacgggctttgtacatctggacctccattttcttctccatatactt
 ttgtaccatcatcttatectcagcaacaaccaacatccttgggtccaaccaattctcagatgcagtagct
 ggcgtccctccagcagcaaacacttggcctgttcctgttaatcaaagcacatcacttgtttccctgtgca
 gcagactgggcaacaaacacccggtcgcagtttccacagacccaggaaacttgactccgcaatctgcactctg
 actggcaggagcatacatctgctgatgggagaaaggctgatgcacactgtatggaaggaatttacaaca
 cctgaaggaaagaaatattattataacaagggttacaaggagctctaagtggacaattccggaagattttaa
 gttagctcgggaacaagcccaactagctagtgaacaaacgtccctttcgggaagctggatctacccctctat
 ccacatgctgcacctcgtctgatctagcagtttagcactgtgacttctgttgttccagcacatcttca
 gcacttactggacattcttcaagccctattcaagcgggtttggctgtacctgtcaccgctcctccctctgt
 tgctcctgttactccaacatctggtgcaattagtgcactgaggctactacaatgtactatttttcttgg
 gaagttttgctgagaataaggaaatgtctgtgaatggaaaagccaatttgtcacctgctggtgacaaagca
 aatgtcgaggaacctatggtatgtactaagcaggaggccaaagctgctttcaagctctcttttggaaatc
 tgtaaattgttcattccgactggacatgggaacagacattgaaagagattgttcacgataaaaagatatggtg
 ctttgaggacactcggcgagcggaaacaagcgttttaacgagtatcttggccaaaggaaaaaagtggaagct
 gaggaaagacgaaggaggcagaagaaagctcgggaagaatttgtcaagatgctagaggagtggaagaact
 ttcatcctccctgaaatggagcaaaagcaatgagtttgttcgaaaatgatcagcgtttttaaagctgttgacc
 gtccataggatcgtgaagatctttttgacaattacattgttggaaacttgagaggaaggaaagagaaaaaggca
 gcggaggaacatcggcagtagtatatggcagactatcggaaagtttcttgaaacctgtgactatatcaaagctgg
 tacacaatggcgcaaaattcaagatagactggaggatgatgacagatgctcatgtcttgaaaagatagatc
 gtctgattgggttttgaggaatacattcttgacctagagaaggaaagaagaagagctgaagagagtagagaaa
 gaacatgtaaggcgggcccagagagaaaaaacctgatgcatttctgtacactattggaagaacatgttgctgc
 aggcacaccttacagccaagacgtactggttggattattgcattgagttaaaaagacttgccccaataaccaag
 ctggtgcatctaatacatctggttcaactccgaaagacttggttgaagatgtcacagaagaattagagaag
 cagtatcatgaggataagagctatgtgaaggatgctatgaagtcaagaaag-----

in CDC2bDN-IC57: atttccatggtctcctcgtg

-----gcaaattttaaatctgctattttcagaagatctcagtagtcaacagatatcagacataaatttaa
 gctggtttgaag in CDC2bDN-IC57

agcttatatatgatgacttggttgggagagtgaaaggaaaaagaagaaaaagaggccagaaagcttcagcgt
 ctggctgaagaattttaccaatctgttgcacactttcaaggaaatcacctagcttcaaattgggaagatag
 caaacaactagtagaagaaagtcaagagtagacagatcgattggagatgaaagtgttagccaagggttatttg
 aggaatacataacgagttttacaagaaaaggcaaggagagaaggagcgttaagcgtgacgaggaaaaaggttaga
 aaagagaaggaaaaggacgagaaagagaaacggaaagacaaggataaggagagaagggaaggaagaga
 acgtgaaaaagagaagggaagagagagtagtaaacgggaagaatcagatggtgagactgctatggtatgtga
 gcgaaggtcataaagacgagaaaaaggaagggaagagatcgtgacagaaaaacatcgaagacggcatcacaac
 aattctgatgaagatgttagttctgataggatgacagagatgagtcgaagaaatcatcccgtaaacatgg
 taatgatcgcaaaaaatcaagaaagcacgcaaacctgcctgaatcgagagtgaaaaacgggcataaaagac
 agaaaaaagagagtagtcgccgaagtggtaatgacgagctagaggatggagaagttggggagtgatagtgga
 aattcgacattaatctgaaacctt

FIGURE 7

8/65

CCP molecule: CCP6: amino acid sequence: (CDC2bDN-IC57):

MANNRRQSSGTQGQHEFVPAASQPFHPYGHVPPNVQSQPRQYSQPIQQQQQLFPVVRGQPVHITSSS
 QAVSVPIYIQTNKILTSGSTQPPNAPPMTGFATSGPPFSSPYTFVPSSYPQQQPTSLVQPNQMH
 VAGVPPAANTWVPVPVNSTSLVSPVQQTGQQTTPVAVSTDPGNLTPQSASDWQEHTSADGRKADAS
 TVWKEFTTPEGKKYYYNKVTKESKWTIPEDLKLAREQAQLASEKTSLSSEAGSTPLSHHAASSSDL
 AVSTVTSVVPSTSSALTGHSSSPIQAGLAVPVTRPPSVAPVPTPTSGAISDTEATTMYFSLGSFA
 ENKEMSVNGKANLSPAGDKANVEEPMVYATKQEAQAAFKSLLESVNVHSDWTWEQTLKEIVHDKR
YGALRTLGERKQAFNEYLGQRKKVEAEERRRRQKKAREEFVKMLEECEELSSSLKWSKAMSLFEN
DQRFKAVDRPRDREDLFDNYIVELERKEREKAAEEHROYMADYRKFLETCDYIKAGTQWRKIQDR
LEDDDRCSCLKIDRLIGFEEYILDLEKEEEEELKRVEKEHVRRRAERKNRDAFRTLLEEHVAAGIL
TAKTYWLDYCIELKDLPOYQAVASNTSGSTPKDLFEDVTEELEKQYHEDKSYVKDAMKSRK
 AN-----FKSAISEDLSLSTQQISDINLKLIYDDLVRVKEKEEKEARKLQRLAEFTNLLHT
ISMVSSWLFE in CDC2bDN-IC57
 FKEITVASNWEDSKQLVEESQEYRSIGDESVSQGLFEEYITSLQEKAKEKERKRDEEKVRKEKER
 DEKEKRKDKDKERREKEREREKEKGKERSKREESDGETAMDVSEGHKDEKRKGKDRDRKHRRRHH
 NNSDEDVSSDRDDRDESKSSRKHGNDRKKSARKHANSPESESENHRHKRQKKESSRRSGNDELEDG
 EVGE

FIGURE 8

9/65

A.

CCP molecule: CCP7/CCP8 nucleotide sequence (CDC2bDN-IC62/E2F3ca55):

tgaacctagattttctgcaactgaattcctaattcgaaaaagaatggaggggttcgtcgtcgacga
 tagcaaggaagacatgggaactagagaacagcattctaacagtagactcacctgattcaacctcc
 gacaacatcttctactacgacgatacttcacagactagggttcagcaagagaaaaacgtgggagaa
 tgatcctcactactttaaacgagtcgaagatctcagcgctcgtctcttctaagatgggtggttcacg
 ctgctctggtggtacaattgaaataatgggtcttatgcaaggtaagaccgatgggtgatactatc
 attgttatggatgcttttgctttaccagtggaggtactgagacaaggggtaatatgctcaggatga
 tgcttatgagtacatgggttgagtattcacagaccaacaaagctcgcggggc-ggctggagaatggt

in CDC2bDN-IC62: c

- in E2F3ca55

gttggatgggtatcactctcaccctggatatggatgctgggtctccggtattgatgtttctacgca
 gaggttaaccaacagcatcaggagccatttttagctggttattgatccacaaggactgttt
 cagctggtaagggttgagattggtgctttcagaacatactctaaaggatataag--cctccagatg

in CDC2bDN-IC62: agc

in E2F3ca55: g--

aacctgtttctgagtatcaaa-ctattcctttaaataagattgaggactttggtgttcaactgcaa

a in CDC2bDN-IC62

- in E2F3ca55

acagtactattcattagatgtcacttatttcaagtcattctcttgattctcaccttctggatctac
 tatggaacaagtaactgggtgaacactctttcttcttctccactgctgggtaatggagactatggt
 gctggacaaatacagacttagctgagaagcttgagcaagccgagagtcattctggttcagtctcg
 ctttgaggaggttgtgccatcatcccttcataagaaaaaagaagatgagtcctcaactaactaaga

g in E2F3ca55

taactcgggtagcgcaaagataactgtggaacaggtccatggactaatgtcgcaggtcataaaa
 gatgaattattcaactcaatgcgtcagtcacaacaacaatctcccactgactcgtcggatccaga
 ccctatgattacatatggaagttgctctttcttttgggtttctanttttggattgacctatcatttg

in E2F3ca55: g

ttgtcctttcattttattttctggttggtgtaaagaattataatgctaatacagaagaaga
 gattttggttaaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP7/CCP8 amino acid sequence (CDC2bDN-IC62/E2F3ca55):

MEGSSSTIARKTWELENSILTVDSPDSTSDNIFYDDTSQTRFQOEKQWENDPHYFKRVKISALALLKMY
 VHARSGGTIEIMGLMQGKTGDTIIVMDAFALPVEGTETRVNAQDDAYEYMVEYSQTNKLAGRLNVVGW
 YHSHPGYGCWLSGIDVSTQTLNQHQEPFLAVVIDPTRTVSAGKVEIGAFRTYSKGYKPPDEPVSEYQTI
 PLNKIEDFGVHCKQYYSLDVTFKSSLDLHLLDNLWNYWVNTLSSSPLLNGNDYVAGQISDLAEKLEQA
 ESHLVQSRFGGVVPSSLHKKKEDESQTKITRDSAKITVEQVHGLMSQVIKDELFSMRQSNKSPDSS
 DPDPMTY

FIGURE 9

10/65

A.

CCP molecule: CCP9 nucleotide sequence (CDC2bDN-IC9):

ggcagcagctctctctctctctctggagcgttctctctctctccttgagcttctcttaccgccattaga
gctccttcacaaactcataaacctatttggttgagccaggcttggttaaccactggcctttttcc
agactaaattatgtattgctctctctctogattgcatccaaatgcaaacaaagaaaatatctctactt
cagatgtacaggagaggttttgtacgaataacgagatcacgagctaaaaaagccatgggaagagga
gtatcaatacctccaacaaaaccttcttttaaacagcaaaaagagacgtgcagtacttaaggatgt
gagtaatacctctgcagatatattttattcagaacttcgaaagggaggcaacatcaaggcaaaaca
gaaaatgtctaaaagagcctaaaaaagcagcaaaaggaaggtgctaacagtgccatggatattctg
gtagatatgcatacagaaaaatcaaaaattagcagaagatttgtccaagatcaggatggctgaagc
ccaagatgtctctctttcaaacttttaagatgaagaaattactgagcaacaagaagatggatcag
gtgtcatggagttacttcaagttgtagatatattgattccaacgtcgaagatccacagtggttgagc
ttgtatgctgctgatataatgacaacatacatgttgagagcttcaacaacgaccttggttaa
ttatatggagcttgtgcagcagagatatcgacccagacatgagaaagattctgattgactggcttg
tagaagtttctgacgactacaagctggttcagatacgtttaccttacagtgaatcttatcgac
cgttttctgtccaacagttacattgaaaggcaaaagactccagctccttggtgtctcttgcatgct
tatagcttcaaaatatgaagagctttccgcaccaggggtggaggaggttttgcttcattacggcca
acacatacacaagacgagaagtgtgagcatggagattcaaattctaaattttgtgcacttttaga
ttatcgggttcctaccaccaaaccatttctgaggcgggttcattaaagcagctcaagcttcgtacaa
ggtgcctttcattgaactggagttatttagcaaaactatctcgccgaattgacactggtggaatata
gtttcctaagggttcctgcccatacctaattgtctgcttcagctgttttctagcccagatggacactc
gaccaaactgaccatccttggaaccctactctgcaacactacaccagatatgaggtgagctgagct
gaagaacacagttctcgccatggaggacttgagctcaacaccagtggtgtactctcgctgcc
cccgtgagaaatacaaccaaccaagtttaagagcgtggcaagctgacatctcccaaaccaggtc
acattactattctcaagatgacaccaagcaacatcgaaaacagagcccaagtcaggtgatcaaaa
tacctattttcagacattggatggttatgtcgtctctttgccagttttgtctgtctgtaattctgt
agctattgtgtggcgcttaattgtaggccattacttgtcacaccacttagctttaataaatgt
tatggaatttttctaategcattgctacaactatttactatcctgcgggattttgtacctaggag
cacttggaacgaatacaaaaagtgttaattaataataaatttcactgttcatggcaaaaaaa

B.

CCP molecule: CCP9 amino acid sequence (CDC2bDN-IC9):

MYCSSSMHPNANKENISTSDVQESFVRI TRSRAKKAMGRGVS I PPTKPSFKQKRRAVLKDVSN
SADIIYSELKGGNIKANRKCLKEPKKAAKEGANSAMDILVDMHTEKSKLAEDLSKIRMAEAQDV
SLSNFKDEEITEQQEDGSGVMELLQVVDI DSNVEDPQCCSLYAADIYDNIHVAELQQRPLANIME
LVQRDIDPDMRKILIDWLVLEVSDDYKLVPDTLYLTVNLI DRFLSNSYIERQRLQLLGVSCLIAS
KYEELSAPGVVEEFCFITANTYTRREVL SMEIQILNFVHFRLSVPTTKTFLRRFIKAAQASYKVPF
IELEYLANYLAE LTLVEYSFLRFLPSLIAASAVFLARWTL DQTDHPWNPTLQHYTRYEVAELKNT
VLAMEDLQLNTSGCTLAATREKYNQPKFKSVAKLTSPKRVTLLFSR

FIGURE 10

11/65

A.

CCP molecule: CCP10 nucleotide sequence (CKSBC001):

cgacatcttctaagaaagaaacaaagaaagacttcacatctttaccattatcttgcctgagctcag
taggagaggttcaagaaacaatggaagatgcaattatcaatctttatcgctgtcggttgcgctta
tcgtctgctctgcatctgctaaaaccgcaagccctccagctccagtgtgcccaccgacaccagct
ccagcaccagccccggaaaatgtgaatctcaccgagcttttaagtgtagctgggtccgttccacac
attcctcgactaccttctctcgactggagtcattgagactttccaaaaccaagctaacaacactg
aggaaggcatcacaatctttgtccctaaagatgatgctttcaaagctcagaagaatcctcctttg
tcaaatctcacaaggatcagcttaagcagcttggttctcttccatgctctgcctcattactattc
gctttcgggaattcaagaacttgagccaatctgggtccagtgtgacacctttgctgggtggtaatact
ccttgaaattcactgatgtttctggcacgggttaggattgattctttatggaccaggactaaagtc
agcagcagtggttttctccactgaccctgttgcggtttaccaagtgaaccgcgtgcttctaccga
agcaatctttggtactgatgtccctccaatgcctgctccagctcctgctcctatcggttagtgctc
cttcggattctccttcagttgctgattctgaaggagcttcttcaccaaagtcctcacacaagaac
tccggacaaaagctgctacttgacccaatctccatgggttatttccggtttggtggcatgtttctt
gtgatcagatgggtttgacagattgagttatgtttttaagttacaatgtgaaagattgtattacat
catttgaattgtctttttgatttttgaaaccattttttattatacatttttatcattattattg
tttgtcattacgattgttgtgaattgaaattgttcctccaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP10 amino acid sequence (CKSBC001):

MAKMQLSIFIAVVALIVCSASAKTASPPAPVLPPTPAPAPAPENVNLTELLSVAGPFHTFLDYLL
STGVIETFQNQANNTTEGITI FVPKDDAFKAQKNPPLSNLTKDQLKQLVLFHALPHYYSLSSEFKN
LSQSGPVSTFAGGQYSLKFTDVSQTVRIDSLWTRTKVSSSVFSTDPVAVYQVNRVLLPEAIFGTD
VPPMPAPAPAPIVSAPSDSPSVADSEGASSPKSSHKNQKLLAPI SMVISGLVALFL

FIGURE 11

12/65

A.

CCP molecule: CCP11 nucleotide sequence (CKSBC011):

cttaaactacatttatcattacagtctgatttgagctaagttctctcatcataaactctccttgg
agaatc**atggctatttcaaaagctcttatog**cttctcttctcatatctcttcttgttctccaact
cgtccaggctgatgtcgaaaactcacagaagaaaaatggttacgcaaagaagatcgattgtggga
gtgctgtgttagcacggtgcaggctttcgaggaggccgaggctgtgtcacagagcgtgcgggac
ttgctgctacagggtgcaactgtgtgcctccgggtacgtacggaaactacgacaagtgc**caagtgct**
acgctagcctcaccacccacggtggacgccgcaagtgccca**ta**agaagaaacaaagctcttaatt
gctgcggataatgggacgatgtcgttttgtagtattttactttggcgtatatatgtggatcgaat
aataaacgagaacgtacgttgtcgtttgtgagtgtagtactgtattattaatggttctattttgtt
tttacttgcaagttttcttgttttgaatttggttttttcatattttgtatatcgattcgtgcatta
ttgtattatttcaatttgtaataagattatgttacctttgagtgggtgtttaaaaaaaaaaaaaa
aaaa

B.

CCP molecule: CCP11 amino acid sequence (CKSBC011): SEQ ID NO:77

MAISKALIASFLISLLVLQLVQADVENSQKKNGYAKKIDCGSACVARLQAFEEAEAVSQSVRDLL
LQVQLCASGYVRKLRQVPVLR

C.

CCP molecule: CCP11 amino acid sequence (CKSBC011): SEQ ID NO:110

MAISKALIASLLISLLVLQLVQADVENSQKKNGYAKKIDCGSACVARCRLSRRPRLCHRACGTCC
YRCNCVPPGTYGNYDKCQCYASLTTHGGRRKCP

FIGURE 12

13/65

A.

CCP molecule: CCP12 and CCP13 nucleotide sequence (CKSBC98-7 C-term and N-term, respectively):

agatggggaagaagaacaagagaagtccaagacgagctctgagctcgaattggagccagagctaacg
aaaataatcgatggagactctaaaaagaagaaaaataagaataagaagaagagaagccatgaaga
tacggagatagaaccggagcaaaaagatgagctctcgacggagactcgagggaggagaagataaaga
agaagaggaagaacaagaaccaagaggaggagccagagcttgtgacggagaaaaacgaaagtccaa
gaggaggaaaaagggaaatgtagaagagggtagagccactgttagcatagccatagctgggttcaat
catccacaacactcaatcacttgagctcgccacacgcgtaattctctcttctctctatctctccc
ttcgtttctctgtttttccattcccagataatttaaagtcaccttcttccatttctaactttct
cagctcgccggccaaattgctcgtgcagctacaattttccgaatcgacgagatcgtagtggtcga
caataagagcagctcagaaatcgaatcagctgctacgaatgcttctgatagcaatgaaagtgggtg
cctcctttctcgttcgtatcttgaagtatctagagacaccacaatatattgaggaaatctctcttc
cccaagcaaaatgatcttagatatgtgggtatgttgccgggtatgttgccacctcttgatgctcc
taccatctgcgtaagcacgagtggaacaataccgtgaagnnnnnattgttccaccctctaagc
caagggagaagcaggaatgtattggggatacaaaagtacgatatgcatcacaattaa

= in CKSBC98-7 C-term

gttcagtattcaaggaatgccctttcgaggggtggttacgattatttgattggtacctcggagcac
ggcctggtaattagttcatctgagctgaaaataccaacatttaggcacctattgattgcatttgg
tggacttgctgggcttgaagaaagtattgaagatgataatcagtataaggggaaaaaacgttcgag
atgtgtttaatgtatacttgaatacttgtccacatcaaggtagccgaaccattcgagcagaggaa
gcgatgtttatatcacttcagtaacttccaggaacccatcagcagggcagtgagaagactttaagc
ttcgataaaaaagaggtcaaaagaagctattttgttctcatagatctgaggtttgtctgaaaaagagt
gatgtaatgtaactgttttagaaaaa

B.

CCP molecule: CCP12 and CCP13 amino acid sequence (CKSBC98-7 C-term and N-term, respectively):

MGKKNKRSQDESELELEPELTKIIDGDSKKKKKNKNKKKRSHEDTEIEPEQKMSLDGDSREEKIKK
KRKNKNQEEPELVTEKTKVQEEKGNVEEGRATVSIAIAGSIIHNTQSLELATRVISLSLYLSL
RFSVFPPFDNLKSPSSISNISQLAGQIARAATIFRID EIVVFDNKSSSEIESAATNASDSNESGA
SFLVRILKYLETPQYLRKSLFPKQNDLRYVGMLPGMPLPPLDAPHHLRKHEWEQYREXXIVPPSKP
REEAGMYWGYKVRYASQLSSVFKECPFEGGYDYLIGTSEHGLVISSSELKIPTFRHLLIAFGGLA
GLEESIEDDNQYKGKNVRDVFNVLNTCPHQGSRTIRAEEAMFISLOYFOEPISRVRRL

FIGURE 13

14/65

A.

CCP molecule: CCP14 nucleotide sequence (CKSBC103-19):

atggaattgcttgacatgaactcaatggctgcctcaatcggcgtctccgtcgcggttctccgttt
cctcctctgtttcgtcgcacgataccaatctcatttttatggcgattcatcccgagtcgactcg
gtaaacacatatactcagctgcttctggagctttcctctcttatctctcctttggcttctcctca
aatcttcacttccttgtcccaatgacgattgggttacgcttcaatggcgatttatcgacccttgtc
tggattcattactttcttcttaggcttcgcttatctcattggctgtcatgtgttttatatgagtg
gtgatgcttggaaagaaggaggaattgattctactggagctttgatgggtattaacactgaaagtg
atttcgtgttgcgataaactacaacgatggaatgttgaaagaagaaggtctacgtgagggtcagaa
gaagaaccgtttgattcagatgccttctcttattgagtactttgggtattgacctctgttgtggaa
gccatttcgctggcccggttttcgaaatgaaagattatctcgaatggactgaagagaaaggaatt
tgggctgtttctgaaaaaggaaagagaccatcgccttatggagcaatgattcgagctgtgtttca
agctgcgatttgtatggctctctatctctatattagtagctcagtttccgttaactcgggttactg
aaccagtgtaccaagaatggggattcttgaagagatttgggtaccaatacatggcgggtttcacg
gctcgttggagattactttatatgttctatctcagaggcttctattattatctctgggttggg
tttcagtgggttgactgatgaaactcagacaaaggctaaatgggaccgcgctaagaatgtcgata
ttttgggggttgagcttgccaagagtgcggttcagattccgcttttctggaacatacaagtcagc
acatggctccgtcactacgtatatgagagaattgtgaagcccggaagaaagcgggtttcttcca
attgctagctacgcaaaccgtcagtgctgtctggcatggactgtatcctggatacattatattct
ttgtgcaatcagcattgatgatcgatgggttcgaaagctattttaccggtggcaacaagcaatacct
ccgaaaatggcaatgctgagaaatgttttgggttctcatcaatttcctctacacagtagtggttct
caattactcatccgtcgggttcatgggttttaagcttgcacgaaacactagtcgccttcaagagtg
tatattacattggaacagttatacctatcgctgtgcttcttctcagctacttagttcctgtgaag
cctgttagaccaaaagaccagaaaagaagaacaatgttgtctttttaaaaaatcaacaacattttg
gttcttttctttttttccacttggncggttttatgtaaaacaagagaaatcaagatttgaggttt
tattcttaaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP14 amino acid sequence (CKSBC103-19):

MELLDMNSMAASIGVSVAVLRFLLCFVATIPISFLWRFIPSRLGKHIYSAASGAFLSYLSFGFSS
NLHFLVPMITIGYASMAIYRPLSGFITFFLGFAYLIGCHVFYMSGDAWKEGGIDSTGALMVLTLKV
ISCSINYNDGMLKEEGLREAQKKNRLIQMPSLIEYFGYCLCCGSHFAGPVFEMKDYLEWTEEKGI
WAVSEKGRPSPYGAMIRAVFQAAICMALYLYLVPQFPLTRFTEPVYQEWGFLKRFQYQYMAAGFT
ARWKYYFIWSISEASIIISGLGFSGWTDETQTKAKWDRAKNVDILGVELAKSÄVQIPLFWNIQVS
TWLRHYVYERIVKPGKKAGFFOLLATQTVSAVWHGLYPGYIIFFVQSALMIDGSKAIYRWQQAIP
PKMAMLRNVLVLINFLYTVVVLNYSSVGFMVLSLHETLVAFKSVYYIGTVIPIAVLLLSYLVPVK
PVRPKTRKEE

FIGURE 14

15/65

A.

CCP molecule: CCP15 nucleotide sequence (CKSBC199-20):

ttatataacctatctacactttgatctccgacaattcactttccaataagaaccaactgagaga
 gagagagcgccggagaagaagaatttttagagagcgatcgacgagggaggttatagcaggtttccgcc
 atggatgctttcgagaagcttgagaaagttggtgaaggacatacgaggaaagtttacagagccag
 agagaaagctaccgggaaaatcgctcgctctaagaagacgcgtctccatgaggacgaagaaggcg
 ttccttccaccactctccgcgagatctccattttgcaatgctcgctcgatcctcacgtcgctc
 aggttaatggatgttaagcaaggactaagcaaagaaggcaaaactgtactgtacctggtttttga
 atacatggacactgatgtcaagaaattcatcagaagtttccgtagcactggcaagaacattccaa
 cccaaactatcaagagcttgatgtatcaactatgcaaaggtatggcattctgccatggtcacggg
 atattgcacagagatctcaagcctcacaatctcttgatggatccaagacaatgaggctcaaaat
 agcagatcttggttttagccagagccttcactctgccaatgaagaagtatacccatgagatattaa
 ctctttggtatagagctccagaggtt-cttcttggtgccacccattactctacagctg
 in CKSBC199.20: ngntt
 tggatatgtggtctgttggtgcatatttgcgaacttgtgaccaaccaagcaatcttt
 n in CKSBC199.20
 caggagagactctgagctccaacagctcctccatattttcaagttggttgggacacccaa
 in CKSBC199.20: -
 tgaagaaatgtggccaggagtgagcacactcaagaactggcatgaataccacagtggaaccat
 cgactctatcctctgctgttccaaacctcgacgaggtctggagttgatcttcta
 - in CKSBC199.20
 tctaaaatgctgcagtagcagccagcgaaacgaatctcagcaaagatggctatggagca
 a in CKSBC199.20
 tccttactttgatgatctgccagaaaagtcctctctctaaaggatttaaaatcttcagtttagtata
 tttccaagttttatggtttttctagttttgcttcttcaagcatatctctagtgtgctgcttccc
 cctctatgaa

B.

CCP molecule: CCP15 amino acid sequence (CKSBC199-20):

MDEGVIAVSAMDAFEKLEKVCECTYGVYRAREKATGKIVALKKTRLHEDEEGVPSTTLREISIL
 RMLARDPHVRLMDVKQGLSKEGKTVLYLVFEYMDTDVKKFIRSFIRSTGKNIPTQTIKSLMYQLC
 KGMAFCHGHGILHRDLKPHNLIMDPKTMRLKIADLGLARAFTLPMKKYTHEILTLWYRAPEVLLG

 ATHYSTAVDMWSVGCIFAELVTNQAI FQGDSELQQLLHIFKLFGTPNEEMWPGVSTLKNWHEYPO
 *** ** * * *****+ + +++++ ++ ++ +++ + +++++ +
 11111 1
 WKPSTLSSAVPNLDEAGVDLLSKMLQYEPAKRISAKMAMEHPYFDDLPEKSSL
 + - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 1 11 1 1 1111 1 1 11 1 1 1 111 1

FIGURE 15

16/65

A.

CCP molecule: CCP16 nucleotide sequence (E2F5BBC1):

tagtcaacgatggatttgagacatgaacaactaattgatttgatttcgtgtagctaactttgtta
 attggtaaattgtgtagagaaggatgagtagtgagtagtgagttgtttgtcactccagagaagcag
 aggcaacatccttcagtgagcgttgagaaaactccagtgagaaggaaattgattggtgatgatga
 ttctgaaattggatcagagaagaaagggcaatcaagaacttctggaggcgggcttcgtcaattca
 gtggttatggtttgtcagaagttggaagccaagaagataactacttacaaggaggttgcagacgaa
 attatttcagattttgccacaattaagcaaaacgcagagaagcctttgaatgaaaatgagtacaa
 tgagaagaacataaggcggagagtgctacgatgcgctcaatgtgttcattggcgttgatattattg
 caagggataaaaaaggaaatccggtggaaaggacttctattacctgcaaaaaggatgtggaagaa
 gtcaagatggatcgtaataaagttatgagcagtggtgcaaaaagaaggctgttttcttaaagagtt
 gagagaaaagggtctcaagtcttgagagtgcttatgtcgagaaatcaagagatggttgtgaagactc
 aaggcccgagcagaaggatttaccttaccattcattctacttgagacaaaccctcacgcagtagtc
 gaaatcgagatttctgaagatatgcaacttgtaacacctcgacttcaatagcacacctttctcggt
 ccatgatgatgcttacattttgaaactgatgcaagaacagaagcaa

in E2F5BBC1: g

gaacagaacagagtatcttcttcttcatctacacatcaccaatctcaacatagctccgctcattc
 ttcattccagttcttgcatgtgcttctggaacctcaggcccggtttgctggaactcgggattccattg
 atactcgcctgaccgagcttctattcccaaattcttcaagaagaagaagtaatgatctaattggta
 tactaaaaaattatacatctggttttagtggtcaattgagagagactgtaaaatcaattcataggc
 caacaaatgtttgtttatccaattttcctttttattcgaacttgatgcatatttcaacggaac
 agaaactattgttttaaaccaaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP16 amino acid sequence (E2F5BBC1):

MSMEMELFVTPEKQRQHPSVSVEKTPVRRKLIIVDDDSEIGSEKKGQSRTS GGGLRQFSVMVCOKL
EAKKITTYKEVADEITISDFATIKQNAEKPLNENEYNEKNIRRRVYDALNVFMALDI IARDKKEIR
 WKGLPITCKKDVEEVKMDRNKVMSSVQKKAFLKELREKVSSLESLSMRNQEMVVKTOGPAEGFT
LPFILLETNPHAVVEIEISEDMOLVHLDENSTPFSVHDDAYILKLMQEQKQEQNRVSSSSSTHHQ
 SQHSSAHSSSSSCIASGTSGPVCWNSGSIDTR

FIGURE 16

17/65

A.

CCP molecule: CCP17 nucleotide sequence (FL67BC4-2):

caaattctctggaagaagaagaagacgaagatgcaaccgacagagacgtcgagccggcgccgctc
ggatcaaggccgcccggcttaaggatcagttatcggagagtatgagcttcagtagccaaatgaaga
aggaagacgatgagttgtcgatgaaagctttgtcggcgttcaaggccaaagaaggagatcgag
aagaagaagatggagatcagagaaagagttcaagctcagcttggtcgtggtgaagatgagtccaa
gcgtctcgctatgattcgcgaggaacttgaagggttttgcgtgatcccatgaggaaggaagttacta
tggtgaggaagaagattgattctctcgacaaagaattaaagccattggggaatacagttcagaaa
aaggaaacagagtacaaggatgctcttgaagcattcaatgaaaagaacaaggagaaggtggagct
gatcaccaagctacaggagttggagggagaaaagcgagaaattcaggttcaagaagctggaggagc
taagcaagaacattgatctaaccaaaaccttagtgttggacgagcagagtcgctgggatttggcta
ttcaaagttctaaaaaagtcacttttttagagtattttcattgttcttttatgattctagtaatat
atataattttataaaaataaaaagtaagaagatatgtgtttgaactagatgttgcaaagaaaatgta
acaaagttacgatggcactacattatcgacgtgattggcagaattgtaatagtaatgtaaagaaa
ctatgtttgttccggaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP17 amino acid sequence (FL67BC4-2):

MQPTETSQPAPSDQGRRLKDQLSESMSSFSSQMKKEDDELSMKALSAFKAKEEEIEKKKMEIRERV
QAQLGRVEDESKRLAMIREEELEGFADPMRKEVTMRKKIDSLDKELKPLGNTVQKKETEKDALE
AFNEKNKEKVELITKLQELEGESEKFRFKKLEELSKNIDLTKP

FIGURE 17

18/65

A.

CCP molecule: CCP18 nucleotide sequence (FL67BC12-17):

atgaaatagggaaaagttagtgaagatggctaacactgtccgcactggcggaaaggggacagtaag
aagaaagaagaaggctgttcacaagaccactacaaccgatgacaagagggtccagagcactctta
agagagttggagtcaattccattcccgccattgaagaagttaacatttttaaggatgatgtagtc
attcagttcattaaccctaaagtccaagcttcaattgctgctaacacatgggttgtagtggtac
accacagacgaaaaaattgcaagacattcttcctcagattatcagccaacttggaccagataact
tggaacaacctgaagaagctagcagagcaattccagaaacaagctccagggtgcaggatgatgtccca
gcaacaatccaagaagaggacgatgatgatgtcccagatcttgtagtgggagagactttcga
gaccctgtctactgaagagggtcccaaa**gctgctgcttcttagaggaggaggaagaagaaggaga**
agagctcacctgcaaaacccatcataaaaatgtttgtcgctcgacctcttctgagcactgtcaga
ttcttgttttctctaattgcttgcgaaacagaaagacttgggttttattatcacttgatgcttttgg
tccgaacagcaattttccttttattaagggttagatcgctttttgtttaccacctgttcaaatgag
tactactatgtcctgtcgcttcatacacttcttgcaacacagtcctttgttttgagtcaaaaaaa
aaaaaaaaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP18 amino acid sequence (FL67BC12-17):

MNREKLMKMANTVRTGGKGTVRRKKKAVHKTTTTDDKRLQSTLKRVGVN SIPAIEEVNIFKDDVV
IQFINPKVQASIAANTWVVS GTPQTKKLQDILPQIIISQLGPDNLDNLKKLAEQF**QKQAPGAGDVP**
ATIQEEDDDDDV PDLVVGETFETPATEEAPKAAAS

FIGURE 18

19/65

A.

CCP molecule: CCP19 nucleotide sequence (JUT1):

tatccggtgaccttatcccctcgccggtgagcgaatctcagatccaaaattttgcaaaatcctcagatcgctcttaccttctccgaatcgatcgatttttcatgaggagacgacgacgagattcagtcattccatctccgggagattcttccctttcaccacaagctcctccttctccgccgatttttgccaacaaacgacgtgacggtggccgctcgtgaagaaaccacaaccggggcctttcttctcaatctccgtccatgaacgcttttagcgtttagtggttcatactccttctgtaaccgggtggtggtggtgtagcggaaacagaaacggacgaggaggaggaggaggaagcgggtggtggtggaggaggaagagatgattggttgagcgaagaagctacaaagggttctaatacgaagcttggggagatcgattctctgaaccaggtaaaaggaactttgaagcaacaacattggaaagaagtagctgagattgtgaacaagagtcgtcaatgcaaataccctaaaactgatattcagtgtaagaacagaattgatacgggtgaagaagaagtataagcaagagaaagctaa gattgcttctggtgatggacctagtaaatgggttttcttcaagaagcttgagagtttgattggtggtactacaacattcattgcttcttcaaaagcttcagagaaggctcctatgggaggagctcttgggaatagccgttcgagtatgtttaaacggcaaaactaaaggtaatcagattgtgcagcaacaacaaga gaagagaggctctgattcgatgcggtggcatttttaggaaacgtagtgcttctgagactgagctctg agtctgatcctgaacctgaggcttctcctgaggaatctgctgagagtcctccacctttgcaaccg attcaaccgcttttcgtttcataatgccaaagcggttgaaggtggataagagtgagggtggaggagg tggagttggagatgtggcgaggggcgatacttggaatttacggaagcttatgagaaggcggaaactg ctaagcttaagttaatggcggaactggaaaaggagaggatgaaatttgctaaagagatggagttg cagagaatgcagttcttgaaaactcaattggagataacacagaacaatcaagaagaggaagagag gagcaggcagcgaggagaaaggaggatcggttgatgatgatgatcgcaatggcaagaataacg gcaatgtaagtagctgacaattgaacacacaaatgttcctatgatatttgctatgataagctgga ttttaggttttgatgttggttggttggttattgttactgccttggtgggatgt

B.

CCP molecule: CCP19 amino acid sequence (JUT1):

MEDDDEIQSIPSPGDSSLSPPQAPSPPIIPTNDVTAVVKKPQPGLSSQSPSPMNALALVVHTPSV
TGGGGSGNRNGRGGGGSGGGGGGRDDCWSEETKVLIEAWGDRFSEPGKGTLLKQQHWKEVAEIV
NKSROCKYPKTDIQCKNRI DTVKKKYKQEKAKIASGDGPSKWVFFKKLESLLIGTTTTFIASSKAS
EKAPMGGALGNSRSSMFKRQTKGNQIVQQQEKRGSDSMRWHFRKRSASETESESDPEPEASPEE
SAESLPPLQPIQPLSFHMPKRLKVDKSGGGSGVGDVARAILGFTEAYEKAETAKLKLMAELEKE
RMKFAKEMELQRMQFLKTQLEITQNNQEEEERSRQRGERRIVDDDDDRNGKNNNGNVSS

FIGURE 19

20/65

CCP molecule: CCP20 and CCP21 nucleotide sequence (JUT2 and JUT3, respectively):

aagctttactacttatactcttttgttcctatgggccacggtatcttcttcctcctggccaaaccc
caaccctaatacccgattccacgtctgcctcagattccgattctacttttccctctcaccgcgac
gcgtagacgaacccgactctctcgattccttctcctccatgagtcct

in JUT2 (N-term): n

aactccgacgaacctaatacagacttctaataatcgctcttttctccccctacgcccatttacc
ggtgatgcctcctccgtccgtgcttcatctttcctttaaccaagatcatgctt

in JUT2 (N-term): t t

gcttcgc-tgtcggcactgacccgtggcttc-cggatcccttaattgcgatcccttttcg

c n

a n n

in JUT2 (N-term)

agattttccggcgctgatttcgatcgtggcggtggtgttgagtcgtggagatgcttttc

g in JUT2 (N-term)

agatgcaatatattagccctagttggtggcgacctgatcctcaatatcctcctaataagggtat
gatttgggatgatcaccagggccgatgtatcggaactctctttcaggtccgatgttagatccg
tccggcttaggagggatcggattattgtcgttcttgagcagaagatttttgtctacaatttctct
gacctcaagctgatgcatcagattgaaaccattgccaaaccctaagggtttgtgtgctgtttctca
gggtgttggttctatggttttggatgtccaggtttgcagaaagggtcaagttcggatcgagcact
acgcttctaaacggaccaaattcgtcatg

in JUT3: =

gctcatgattccagaatagcttgcttcgctctcacgcaggatggccatttgttggccactgctag
ctctaagggtactctggttcggatcttcaatactgttgatgggtaccttgcgtaagagctctggca

in JUT3: -----

cttctgaggatgaaataggttaaggaggg-tgcggtatagagcagagat

g in JUT3

ctacagtttggccttctcttcaaatgctcagtggttagctgtctcaagtgacaaaggaacggtcc
atgtctttggtctcaaagtcactccggatctcaagtgaagactcatcccgaattgcacctgat
gctactccctcatccccatcgctcgtctctgtctttattcaa---agt

in JUT3: agg

gttaccgagggtatttcagctcggagtggtcgggtggctcagttcaggttggttgaaggaaactcagt
acatagccgcctttggccatcaaaagaacacggttggtattcttggcatggatgggagcttctac
agatgccagtttgatccggtgaacggcgggtgaaatgtctcagcttgagtaccacaactgtctgaa
accgccttcagttttctaaaagctttactacttatactcttttgttccttctctcttttatatc
tctctgcaacttaagcgggtgagatatggtgtatagttttgtgtatataataatgatgggtcgtcc
tataatttgtaaaaccttttatcgctacccgggtcgactctagagccctatagtgagtcgtatta
ctgcagagatctatgaatcgtagatactgaaaaa

FIGURE 20

21/65

CCP molecule: CCP20 and CCP21 amino acid sequence (JUT2 and JUT3, respectively):

MATVSSSSWPNPNPDPDSTSASDSDSTFPSHRDRVDEPDSLDSFSSMSLNSDEPNQTSNQSPLSP
PTPNLPVMPPPSVLHLSFNQDHACFAVGTDRGFRILNCDPFREIFRRDFDRGGGVAVVEMLFRCN
ILALVGGGPDPOYPNKMVWDDHQGRGIGELSFSDVRSVRLRRDRIIVVLEQKIFVYNFSDLK
LMHQIETIANPKGLCAVSQGVGSMVLVCPGLQKGQVRIEHYASKRTKFVMAHDSRIACFALTQDG
HLLATASSKGTLVRI FNTVDGTLROESGTSEDEIGKEGADRAEIYSLAFSSNAOWLAVSSDKGTV
VRR----- in JUT3
HVFGKLVNSGSOVKDSSRIAPDATPSSPSSSLSLFK-VLPRYFSSEWSVAQFRLVEGTOYIAAFG
G in JUT3
HOKNTVVILGMDGSFYRCQFDPVNGGEMSOLEYHNCLKPPSVF

FIGURE 21

22/65

CCP molecule: CCP22 nucleotide sequence (JUT6):

agagcttcctctctctatatctggccttctctatggatgtaggagttactacggcggaagtctatact
tgagaagcctctgaagcttctcactgaagaagacatttctcagcttactcgcgaagattgccgca
aattcctcaaagagaaagggtttcttcttcttcttcttctccatttttttccgggtcttattgtcttc
gacgaatggcggctgacacgtgtcgaaacaggaatgcgcaggccttcgtggaataaatctcaggc
gatccagcaagttttatctcttaaagctctctatgaacctggagatgattccggcgccggaatcc
tccgcaagatccttggtttctcagccgccaatccgcctcgcgttacaacaacggtgattgagcca
aggaacgagctcgaagcttggtggaaggattcctttacaggaagatgatggtgcgtgccatagaag
ggattctccaagatcagctgagttttctggtagttctggtcagtttggtgcggtataaagatagcc
acaagactgtttctgtttccccagaagccagctgaaacaaatgcggtgggttgggcaaatgacg
atattttatagtggaagtgatgtatatgatggagtaccacctgaaaaggcccggtctatcat
gcattttgagccaatccaattgatttgctgaaaatggtatttttgccttctagtagaatgattt
cgaaacccatgagtaaagagaagatggtggagcttccccaatatggacttgaaaaggcacctgct
tctcgtgattctgatgttgagggtcaggcgaacagaaaagtatcggttgcaaagatatcttgaaaa
gcggaagacagattttctaagaccaagaaggctccaggagttgcgtcctctagcttgagatgt
ttctgaatcgtcagccacggatgaacgctgcataattcacaaaaccttagtggcacagggcattgc
gagtcacctgaaaatcaaacaaaaagtcccaatatctcagttgatctaaacagtgatctaaacag
cgaaggtgccaaaagaactggagatggtactacgggtcaaaaaggcggaagaacaatttcatggt
cttataacatgactaagacatcacgaggaacacgatgggtgaagcgggtcaagagaagaagtgatt
caagcttggtatatggatgatagtgaaaggatcagagacttctcaccacaaggatcctaaaga
gtttgtatcggttggaacaaacttgagagctgggagtacttagctggagacttgatgctgataact
atgaaaccgatgaggatttgaaaaagatccgtgaatctcgtggttactcttacatggacttttgt
gaggtatgcccggaaaagcttccaaactatgaagtgaagtgaaagagctttttcgaagaacattt
acacactgatgaggagatccgttactgcgttgagggaactggttactttgatgtgagagatcgta
atgaagcttgattagggatttggttaaagaaggagggtatgatagtcttacctgctgggatctat
catcgcttcaactgtggactctgacaactatatcaaggcaatgcggctattcgtgggtgaaccggt
atggacaccatacaatcgcccacacgaccatcttcttgcaggaaagaatatgtcgataacttca
tgatcaatgcctcggcttagagagcttctctctctatatctggctttctgaaacaaggatctat
aaacaaggcctacaataaagaaagctttcctgtcaagtattggataattatgtattcctgtgt
agaatgatggcttttgggtatgcttgagttggtgtaaacttagttacactctctgatatgtctctc
tttaccatctttgtcgtatcccatatacgaaaagattacattgggattcatattgtcttacgctc
gttcctatgtgcaatatggtgagtttt

FIGURE 22

23/65

CCP molecule: CCP22 amino acid sequence (JUT6):

MDVGVTAKSILEKPLKLLTEEDISQLTREDCKRFLKEKGFFFFLSPFFSGLIVFDEWRLTRVET
GMRRPSWNKSQAIQQVLSLKALYEPGDDSGAGILRKILVSQPPNPPRVTTTLIEPRNELEACGRI
PLQEDDGACHRRDSPRSAEFSGSSGQFVADKDSHKT VSVSPRSPAETNAVVGQMTIFYSGKVN VY
DGVPEKARSIMHFAANPIDLPENGIFASSRMISKPMSEKEMVELPQYGLEKAPASRDS DVEGQA
NRKVS LQRYLEKRKDRFSKTKKAPGVASSSLEMFLNRQPRMNAAYSQNL SGTGHCESPENQTKSP
NISVDLNSDLNSEGAKRTGDGTTGQKAGRTISCSYNMTKTSRGTRWVKRSREEVIQAWYMD DSEE
DQRLPHHKDPKEFVSLDKLAELGVLSWRLDADNYETDEDLKKIRESRGYSYMD FCEVCPEKLPNY
EVKVKSFFEEHLHTDEEIRYCVAGTGYFDVRDRNEAWIRVLVKKGGMIVLPAGIYHRFTVDS DNY
IKAMRLFVGEPVWTPYNRPHDHLPARKEYVDNFMINASA

FIGURE 23

24/65

A.

CCP molecule: CCP23 nucleotide sequence (kbp1):

catcgcttttcgctgaaatcaaaatttctccagttttccgatcagtcgcaagaaaaccc

c in KBP1

taaaaatcgatgggtcatgattcttaaggataactaagcagagcactgctgatatgactgct

g in KBP1

tttgtccaaaatcttctccagcagatgcaaaccagggttccagacaatgtcggactccatcatcacaaagattgatgacatgggaggcagaatcaatgagctggagcaaagcatcaatgatctaagagccgagatgggagttagaaggcactcctcctccagcctccaaatcaggcgatgaacccaaaaacacgggtagttcctcttaaaaagggaatgtggtgttcattgacatgtccgaaggaaaaagaaaaactatgaaatatgttaagagcagtattacttttaaaattcctgttttaagaaacgagtttgtgtttattaaag

- in KBP1

ttcatcaaatagattgatgatgtggtgcattacattattctccacctatgaattgcatttctattttggtctaaaaaaaaaaa

B.

CCP molecule: CCP23 amino acid sequence (kbp1): SEQ ID NO:89

TSFPITRKKTLKMDGHDS EDTKQSTADMTAFVQNL LQOMQTRFQTMSDSIITKIDDMGGRINELEQSINDLRAEMGVEGTPPPASKSGDEPKTPASSS

C.

CCP molecule: CCP23 amino acid sequence (kbp1): SEQ ID NO:118

MDGHDSKDTKQSTADMTAFVQNL LQOMQTRFQTMSDSIITKIDDMGGRINELEQSINDLRAEMGVEGTPPPASKSGDEPKTPASSS

FIGURE 24

25/65

CCP molecule: CCP24 nucleotide sequence (kbp3):

CPD molecule: CUP24 nucleotide sequence (kbp5).

agaacaattgagattcttgggtgtgttaagatggaatctacaccatgaaaaacgaattttcttgt
actggccttgtcttctgtgtatccttcttcaagcttccatgaggtttcttgcaggatgatggtg
gtggtttgagtaatttgatctaatagaacgtgattatcaagatagtgtaatgctcttcaaggc
aaggacgatgaagatcagctctgcaaagatacagagtgaaaaccagaataacactacagtactga
taagaacactatttctctatctctatcagatgaatctgaggttggatctgttagtgatgaaagcg
ttggacgttcgagctctgttggatcaaactcaaacctgaattcgaagctcatcacaatagtattaac
caagctggatctgatgggtgtcaaggctgaatccaaggatgatgatgaagaattatctgctcatag
acagaaaaatgttggagaagaatcgaacatgagtttgaagctgcttcagatagctctgaaacaactaa
agactgatgatgtaaacgaaggaaatgatgaagaacattctgcaaagaggcaaagtttgttggaa
gagatcgaacgtgagtttgaagctgctacaaagaacttgaacaactaaagggttaatgacttcac
cggggacaaagatgacgaagaacactctgcaaagagaaaaagtatgcttgaagctattgaaacgcg
agtttgaagctgctatggaaggcattgaagcacttaagggttctgattccacaggaagcggagat
gttgagaacaatctgcaaagagactaagtatgcttgaagagatcgaacgggaatttgaagctgc
ttcaaaagggtcttgaacaactaagggttagcgattcaaccgcggacaataacgaagaagaacacg
ctgcaaagggacaaagtttgttagaagagatcgaacgagagttcgaagctgctacagagagcctt
aagcaacttcaagttgatgattctactgaagacaaagaacactgtaaagcactcttcttcttatt
atctgctattcttctctatggttatctgaatcaggccttgaatgtattgtagttacagctgcaa
agaggcaaagtctgctggaagagattgaacgtgaatttgaagctgcaacaaaagatcttaaaacaa
ctaaatgatttcaactgaaggcagtgctgatgatgaacaatctgcaaagagaaaacaaaatgttggg
agatatcgaaacgcaatttgaagctgctacaataggctcttgaacaactaaaggctaatgatttct
ctgaaggcaataataatgaagaacaatctgcaaagagaaagagtatgcttgaagagatcgaacgc
gagttcgaagctgctattggaggtcttaaacagatcaaagttgatgattccagaaatcttgaaga
agaatctgctaagagaaaagataattttggaagagatggaaacgtgaatttgaagaagcacacagtg
gtattaatgcaaaggctgacaaagaagaatctgcaaagaaacagagtggtctgctataccagag
gttcttggactaggacagtcaggtggttgtagctgttctaaacaagacgaagattcctcgattgt
tataccaacaaaatatagcatagaagatatcctctctgaagaatctgcagtcacgggaacagaga
cttctagtctcaccgcgtctttgactcaactcgttgagaatcacaggaaaagaaaaggaatctcta
ctcggacacagagttctcacttctccttctatagcttcttccacaagcgaatcatctgctacatc
agagactgtagaaaccctaagggtctaaactgaatgagcttcgcggcttaaccgctcagtgagctg
tgacacgtaaagatttcggtcagattctcattacggctgcgagttttgaagagctaagttcagct
ccaatcagttacatttctaggttagctaaatacagaaacgtcatcaagaagagacttgaagcttc
tgagagagttcacatcgcgaggtacgagcaaaaatgctcaaagaagttgcccacgggagaagcaaa
ccgccgtggacactcatttcgcaaccgctaaaaagcttgcctcaagaaggagacgcgttgttgcgtt
aaaatcttcgcaatcaagaaaactgttggcgaaacttgaagtcagagagaaagaatctgttgcgtgaa
gtttaaggagactgtgaaagaactttctcattcttctggctgatgcttctgaggttacgaagagt
atcatggcgcggtgaggaaggcgaaagacgagcaagcggctgaggaatttgcgaaagaggcgacg
caaagtcagagatcatttgggttaagtttcttaggttctctttagagaacaattgagattcttgg
ttgtgttaagagcaaatctagagctcttgttgggttcttgttatgtattttgtgatgatgttctgt
ttcagagtttgtgtgttgggtgtatcaggagaaagaggctgggagatagagagaaagagagctctc
tgcgaaaactaataatgttttttcagatatctaataataagctttttacaaaaaaaaaaaaaaaaa
aaaaaaaaaa

FIGURE 25

26/65

CCP molecule: CCP24 amino acid sequence (kbp3):

MEIYTMKTNELVLALSLCILSSFEHVSCQDDGSGLSNLDLIERDYQDSVNALQGKDEEDQSAKI
QSENQNNNTTVDKNTISLSLSDESEVGSVSDSVGRSSLLDQIKLEFEAHNSINQAGSDGVKAE
SKDDDEELSAHRQKMLEEIEHEFEAAASDSLKQLKTDDVNEGNDDEEHSAKRQSLLEEIEREFEEAAT
KELEQLKVNDFGTGDKDDEEHSAKRKSMLEAIEREFEEAAMEGIEALKVSDSTGSGDDEEQSAKRLS
MLEEIEREFEEAASKGLEQLRASDSTADNNEEEHAAKGQSLLEEIEREFEEAATESLKQLQVDDSTE
DKEHCKALFFLLSAILSLWLSESGFECIVVTAARQSLLEEIEREFEEAATKDLKQLNDFTEGSAD
DEQSAKRNMLEDIEREFEEAATIGLEQLKANDFSEGNNEEQSAKRKSMLEEIEREFEEAIGGLK
QIKVDDSRNLEESAKRKIIIEEMEREFEEAHSGINAKADKEESAKKQSGSAIPEVLGLGQSGGC
SCSKQDEDEDSSIVIPTKYSIDILSESAVQGTETSSLTASLTQLVENHRKEKESLLGHRVLTSPS
IASSTSESSATSETVETLRACLNELRGLTARELVTRKDFGQILITAASFEELSSAPISYISRLAK
YRNVIKEGLEASERVHIAQVRKMLKEVATEKQTAVDTHFATAKKLAQEGDALFVKIFAIAKKLLA
KLEAEKESVDGKFKE TVKELSHLLADASEAYEEYHGAVRKAKDEQAEEFAKEATQSAEIIWVKF
LSSL

FIGURE 26

27/65

CCP molecule: CCP25 nucleotide sequence (kbp6):

aatttgaatccaatccccaaattatctcatatcgaggttggatctttcttgtgtccttagggac
atcttttgttatcttcgtcattctcatgcttctcttcacctggcttctcgcaaactctggaaatg
ctccattttattaccggaatcggatccttaaagggctggagccatgggaaggcacctccttgact
cgaaacccttttgcttggatgcgtgaagctttagacttctctgaacaagatgtcgttaacttatc
cggcgtcgatactgctgtccactttgtcttcttgagcactgttctggggatatttggcttgtcca
gtcttcttctcctaccaactctactgcctctagccgctacagacaacaacataaagaacacaaag
aatgcgacagataccacaagcaaaaggaacttttagccaacttgataatctatcaatggctaacat
cacaaaaaaaagtctcgaggctgtggcgcttcttaggagctgtttactggatatcttgggtcacat
atttcttcttgtggaaagcttataagcatgtctcttcattgagagctcaagctctgatgtctgct
gatgtaaaacccgagcaattcgctattcttgttagggatatgcctgcaccacctgacgggagac
acagaaagagtttattgattcttatttcagagaaatataccctgagacattctacagatcgcttg
tcgcaacagaaaaacagcaagggttaataaaaatagggaaaaattggaaggttacaagaagaagctt
gcgcgagcagaagcaatattagcagcaactaataaccgtcccacgaacaaaaccggcttctgtgg
gctagtgcgttaacaagtagacagcattgagtattacactgagctaataacagagctctgtagcca
aactggaaacagagcagaaagcggttcttgctgagaagcagcaaaccgcagcagtggtttcttc
acaaccagggttgctgctgcacagcagctcagctctctgcactgccagatgggttgataaatggac
tgtgaccgaagctcctgagccacggcagctcctatggcagaatctcaacatcaagctcttcagca
gaataatccggcaatacttcatctacttcttgggtgagtgaccattctgttttacatgatacca
atcgcggttcgtctctgccatcaccactcttaagaatcttcagaggattattccggtcataaagcc
gggttgaggagataaccgccataagaaccgttttgaggtcttctcctcctcagattgcgctcattg
tttcttggccatgttgccgaagcttctcttgttctctccaaagccgaggggattccttcacag
agccatgccattagggctgcttcagggaagtaacttttacttctcggtctttaatgtcttcattgg
tgttacccttgctgggactttgttcaacacagtgaaggatatcgcgaaaaatcccaaactcgaca
tgattattaaccttttggctactagcctccctaagagcgcaactttcttctgacctacgttgct
ctcaagttctttatcggttatggccttgagctgtctcggatcatacctttgataatcttccacct
gaaaaagaagtatctctgcaaaaccgaagcggaggtcaaagaagcttggtacccgggagacttaa
gctatgcgactaggggttcccgagacatgtcatcctcacaatcacgttctgctattcagtcatt
gtcctcttatectcatattcggcatacactactttggtttaggctggctagtcctcaggaatca
ggcgttgaaagtgtacgttccatcatacagagactatggaagaatgtggccgcatattcaccagc
gcatactagcagcgttgtttctattccaagtggtaatgtttggctacttaggagccaagacattc
ttctacaacggcccttgatccctctcattatcacctctctcatcttcggatatgtgtgccgcca
gaaattctacggaggggttcgaacacacagctctcgaggtagcttgccgtgagctgaagcagagtc
cagacctagaggagattttcagagcatacattccgcatagcttgagctctcacaaccagaagaa
cacgagttcaaaggcgcaatgtctcggttatcaagatttcaacgcaatagcaggcgtttaagctt
gagagattcctctggctaaaccag

FIGURE 27

28/65

CCP molecule: CCP25 amino acid sequence (kbp6):

MEFGSFLVSLGTSFVIFVILMLLFTWLSRKSGNAPIYYPNRILKGLEPWEGTSLTRNPFawmREA
LTSSEQDVVNLSGVDTAHHEVELSTVLGIFACSSLLLLPTLLPLAATDNNIKNTKNATDTTSKGT
FSQLDNLSMANITKKSSRLWAFLGAVYWISLVTYFFFLWKAYKHVSSLRAQALMSADVKPEQFAIL
VRDMPAPPDGTQKEFIDSYFREIYPETFYRSLVATENSKVNKIWEKLEGYKKKLARAEAILAAT
NNRPTNKTGFCGLVGKQVDSIEYYTELINEsvakLETEQKAVLAEKQOTAAVVFFTTTRVAAASAA
QSLHCQMVDKWTVTEAPEPROLLWQNLNKLFSRIIRQYFIYFFVAVTILFYMPIAFVSAITTL
KNLQRIIPFIKPVEITAIRTVLESFLPQIALIVFLAMLPKLLLFLSKAEGIPSQSHAIRAASGK
YFYFSVFNVFIGVTLAGTLFNTVKDIAKNPKLDMIINLLATSLPKSATFFLTyVALKFFIGYGLE
LSRIIPLIIFHLKKKYLCKTEAEVKEAWYPGDLSYATRVPGDMLILTITFCYSVIAPLILIFGIT
YFGLGWLVLRNQALKVYVPSYESYGRMWPPIHQRIILAALFLFQVVMFGYLGAKTFFYTALVIPLI
ITSLIFGYVCRQKFYGGFEHTALEVACRELKQSPDLEEIFRAYIPHSLSSSHKPEEHEFKGAMSRY
QDFNAIAGV

FIGURE 28

29/65

CCP molecule: CCP26 nucleotide sequence (kbp9):

aacaataagaagaaaaagtttcattttctg~~atg~~gcggagcagaagagtaccaatatgtggaactg
ggaggtgactgggttcgaatcgaagaagtcgccttctagtgaggaaggcggttcacgcgacaccgt
cttctatgcttcgacggtactcgatcccgaagaactcgcttcaccgcactcgctcggagcttgcg
tctaaggttcagagtttgaaggataaagttcagcttgcaaaggacgattatgtgggattgagaca
ggaagctactgatcttcaagagtactccaatgcgaagcttgaaagggttacacggtatttaggtg
ttctggctgataaaagtcgtaaactggatcaatatgcacttgagactgaggctaggatatctcca
cttatcaatgagaagaagagactgttcaatgacttactgacgaccaaaggtgcacatcttccatt
tccgacgtcattctctatccttacttctattgatattgatcacaccagacccttatttgaagacg
agggctccctctatcattgaatttcctgataactgcactatacgcgtaaactagtgatgatact
ctgtccaatcccaagaaggaatttgaatttgatagagtttatgggctcaagttggacaagcttc
actgttcagtgtatgtccaaccttttggtgcaatccgctctggatggatcgaacggttctatatttg
cgtatggccaaactcacgcggggaagacatacaccatgggttgcccctcctttcccttctctct
gaaattagatataggtcttggttggaatttaaataatgataggcaagttcatggacggtcatagtaa
gttcatggacgaaggatctaatacaggacggtggtttatatgctcgttggtttgaggaacttatgg
acttggccaattctgattcaacttccgcatctcagttcagtttctctggttcagtgtttgagctt
tataacgaacaggtcagggatttactctcgggttgctcagagcaatttgccaaagatcaatatggg
tttacgcgaatcggttatagaactttcacaggaaaaagttgataatccatcagagttcatgagag
tcctgaactctgcatttccagaatagagggaatgataaatcaaagtctactgtgacccatctgatt
gtctcgatacacatttgttatagcaacacaattacgagagaaaaatgtaattagcaagctttcttt
agttgacctggctggaagtgaaggtttaactgtggaggatgacaatggagatcatgtaactgatc
tgctccatgtaacaaattcaatttccgcgctgggagatgttttatcatctttgacgtcaaaaaga
gataccattccttacgagaactcatttcttacaagaatacttgagattcactaggagggagctc
caaaacattgatgatcgtcaacatttgtccaagtgcacggaacttgcttgaaataatgtcgtgtc
tcaactatgctgctagagctcgaaatactgtaccaagccttggggaatcgagacacaattaaagaaa
tgagagagcgtggcaaatgatgctcggaaggaggtattggagaaagagaggggaaatcagcgtct
aaaacaagaggttacgggtttaaaacaagcacttaaagaagcaaatgaccaatgtgtactgtct
ataatgaagtacagagagcgtggagagtttattcacactgcaatcagatttaaagtcagagaat
gcgatgggtgtagacaaacataaaaatagaaaaggagcagaattttcagttaaagaaatcaaatagc
tcaacttttacagttagaacaggaacaaaagctgcaggcgcaacaacaagattccaccattcaaa
atctccagttctaaagtgaagacttagaatacacaactaagtaaaagctctgaagtctgacatgaca
agatcgagagatcccttggaacctcagcccagagcagctgagaacacactcgattcttctgcagt
taccagaaaacttgaggaagaattgaaaaaacgtgatgcactgattgagaggttgcatgaagaaa
atgaaaaattgttcgacagattaacagaaaagtcagtggttagctcgactcaggtatctagcccc
tcatcaaaaagcttcaccaacagtgacgctgcagatgttgacaggaaaaatagcgcgggcacttt
accgtcttcagtggtataaaaatgagggcaggttacattagtaaaatccagctctgaattagtaa
aaaccactccagctggagaataacttaacagctgcattgaatgattttgatcccgaacaatatgaa
ggctcttgagccatagctgatggcgcaaaacagcttctgatgctggtcttagcagctgtcataaa
ggctgggtgcttccagagagcatgaaatccttgctgagatcagagattctgtcttttcatttatcc
ggaaaatggaaccaaggagagtaattggatacaatgcttggttctcgagtcaggatattgtacata
aggtccttacttgcacgatcacctgagcttcagtcgatcaaggtttctcctgttgaaacgcttttt
ggagaagccatataactggtcgaactagaagctccagcgggagtagcagcccaggtagatcaccag

FIGURE 29

30/65

ttcgatattatgatgagcagatTTtatggctTTtaaagTTaatTTtaaagccagaaaagaaaagtaag
 ttggtatctgtagTTTcaagaatccgtggacatgaccaggatactgggaggcagcaagtgactgg
 aggaaagctgagggagatacaagatgaagccaaaagTTTTgccattggaaacaaacccttagctg
 ctttattttgttcacactccggctgggtgaactgcaaagacagattaggtcatggcttgcaaaaagt
 tttaggtttctctctgttacagcagatgatgtttcaggagtaaccactggccaattagagcttct
 ttccacagcaattatggatggctggatggctggagtaggagctgcggtgccacctcacacagacg
 ctttaggacagct

c t in KBP9
 tttgtctgagtatgcaaaacgagctctacacttctcagatgcagcatctaaaggatattg

g g in KBP9
 ccggtactttggcttcggaagaggcagaagatgctggtcaagtgcggaagcttcgatcagctctc
 gagtctgttgaccacaaaagaagaaagattttgcaacaaatgagaagtgatgcagctttgtttac
 ctggaagaaggcagttccctgttcaaaatccatctacagcagccgaagactcgagattagcct
 cctcattttctctggatgccatactgaagcaagtcaaggaaataacaagacaagcctctgtccac
 gttttgagtaaaagcaagaaaaaggcattgcttgagtctcttgatgaacttaacgaacgaatgcc
 ttctctgcttgatgttgatcatccatgtgcacagagagaaattgatacggctcaccagttggtcg
 agacaattccagaacaagaggacaatcttcaagacgaaaagagaccttcaatagattcaatatct
 tcgactgaaaccgatgtgtctcaatggaatgttttgcaattcaacacaggaggctcttcagctcc
 attcatcataaaatgcggagctaactccaactcagagctcgtgatcaaagcggatgcccgattc
 aagaacctaaaggaggcgaaatagtgaagttgtgccaagaccttcggttttagaaaacatgagc
 ttagaggaaatgaaacaagtgtttggtcagttgcccgaagctctaagttcactggccttagctag
 aacagctgatggcacacgggctcgatactctagactctacagaactctagccatgaaggttccct
 ctcttagggacctcgttggagagcttgagaaaggaggagtctttaaagatacaaaaatcgacatga
 taggattagggttttttcgtgaatttgaaa

FIGURE 29 (continued)

31/65

CCP molecule: CCP26 amino acid sequence (kbp9):

MAEQKSTNMWNWEVTGFESKKSPSSEEGVHRTTPSSMLRRYSIPKNSLPPHSSSELASKVQSLKDKV
 QLAQDDYVGLRQEATDLQEYSNAKLERVTRYLGVLADKSRKLDQYALETEARISPLINEKKRLFN
 DLLTTKGAHLPFPTSFSILTSIDIDHTRPLFEDEGPSIIIEFPDNCTIRVNTSDDTLSNPKKEFEF
 DRVYGPQVGQASLFSVDVQPFVQSALDGSNVSIFAYGQTHAGKTYTMVAPPFPFLSEIRYRSCDL
 NMIGKFMVDVHSHKFMDEGSNQDRGLYARCFEELMDLANSDESTASQFSFSVSVFELYNEQVRDLS
 GCQSNLPKINMGLRESVIELSQEKVDNPSEFMRVLNSAFQNRGNDKSKSTVTHLIVSIHICYSNT
 ITRENVISKLSLVDLAGSEGLTVEDDNGDHVTDLLHVTNSISALGDVLSLTSKRDTIPYENSFL
 TRILADSLGGSSKTLMIIVNICPSARNLSEIMSCNLYAARANTVPSLGNRDTIKKWRDVANDARK
 EVLEKERENQRLKQEVTLGLKQALKEANDQCVLLYNEVQRAWRVSTLQSDLKSENAMVVDKHKE
 KEQNFQLRNQIAQLLQLEQEQKLQAQQQDSTIQNLQSKVKDLESQLSKALKSDMTRSRDPLEPQP
 RAAENTLDSSAVTKKLEELKKRDALIERLHEENEKLFDRLTEKSVASSTQVSSPSSKASPTVQP
 ADVDRKNSAGTLPSSVDKNEGTTTLVKSSSELVKTTPAGEYLTAALNDFDPEQYEGLAADIADGAN
 KLLMLVLA AVIKAGASREHEILAEIRDSVFSFIRKMEPRRVMDTMLVSRVRILYIRSLARSPEL
 QSIKVSPVERFLEKPYTGRTRSSSGSSSPGRSPVRYDEQIYGFKNLKPCKSKLVSVVSRIRG
 HDQDTGRQQVTGGKLEIQDEAKSFAIGNKPLAALFVHTPAGELQRQIRSWLAESFEFLSVTADD
 VSGVTTGQLELLSTAIMDGWMAGVGA AVPPHTDALGQLLSEYAKRVYTSOMQHLKDIAGTLASEE

P in KBP9

AEDAGQVAKLRSALSVDHKRRKILOQMRS DAALFTLEEGSSPVQNPSTAAEDSRIASLISLDAI
 LKQVKEITRQASVHVLKSKKKALLES LDELNERMPSLLDVDHPCAQREIDTAHQLVETIPEQED
 NLQDEKRPSIDISSTETDVSQWNVLQFNTGGSSAPFIIKCGANSNSELVIKADARIOEPKGGEI
 VRVVP RP SVLENMSLEEMKQVFGQLPEALSSALARTADGTRARYSRLYRTLAMKVPSLRDLVGE
 LEKGGVLKDTKST

FIGURE 30

32/65

A.**CCP molecule: CCP27 nucleotide sequence (kbp11):**

ttagttagatagggcgggtggttggtgcggttcatggcgaatccttgggtgggtaggggaatggttgcgat
 cgggtggagttgagagtcacgtgacgtcatcagctccttcctttgcaccacagaaacagtaacaaca
 acaaccaccgactatgactcggtcggatccaagattggaccatgacttcaccaccaacaacagt
 ggaagccctaataaccagactcagagccaagaagaacagacagagacgagcaaccagctgt
 tgaaccggatccggatccgggtctacgggtcgctcgctcctagaggtagacctcctgggtccaaga
 acaaaccaaagagtccagttggtgttaccaaagaaagccctaactctctccagagccatgttctt
 gagattgctacgggagctgacgtggcggaagcttaaacgcctttgctcgtagacgcggccgggg
 cgtttcgggtgctgagcggtagtggtttggttactaatgttactctgctcagcctgctgcatccg
 gtggagttggttagtttacgtggtcagtttgagatcttgctctatgtgtggggcttttcttcctacg
 tctggctctcctgctgcagccgctgggttaaccatttacttagctggagctcaaggtcaagttgt
 gggaggtggagttgctggcccgcttattgcctctggaccgcttattgtgatagctgctacgtttt
 gcaatgccacttatgagaggttacggattgaggaagaacaacagcaagagcagccgcttcaacta
gaagatgggaagaagcagaaagaagagaatgatgataacgagagtgggaataacggaaacgaagg
atcgatgcagccgccgatgtataatatgcctcctaattttatcccaaatgggtcatcaaatggctc
aacacgacgtgtattgggggtggtcctccgcctcgctgctcctccttcgtattgatta-gttagata
in KBP11 a
 ggcggtggttggtgcggttctttttactggaatgattatattttccattaggatgggttaggctttt
 gtttattaaagctatcaagtttcttttttttttacggataattcggatgacaattagctagtgtt
 - in KBP11 - in KBP11
 tgtttggttgtttgtggc-ggcttttctgacttgactattttgatcgcggtatagctttgtatga
 c -in KBP11
 aagtgaattgattgtagaatcgctcttttgaaattttgatgttgaaaaaaccaagcaatgggtgtgt
ggcctttgcaatggaagc
 n in KBP11

B.**CCP molecule: CCP27 amino acid sequence (kbp11):**

MANPWWVGNVAIGGVESPTSSAPSLHHRNSNNNNPPTMTRSDPRLDHDFTTNNSGSPNTQTQSQ
 EEQNSRDEQPAVEPGSGSGSTGRRPRGRPPGSKNPKSPVVVTKESPNSLQSHVLEIATGADVAE
 SLNAFARRRGRGVSVLSGSLVTNVTLRQPAASGGVVSIRGQFEILSMCGAFLPTSGSPAAAAGL
 TIYLAGAQGQVVGGVAGPLIASGPVIVIAATFCNATYERLPIEEEQQQEQPLQLEDGKKQKEEN
DDNESGNNNGEGSMQPPMYNMPPNFI PNGHQMAQHDVYWGGPPPRAPPSY

FIGURE 31

33/65

CCP molecule: CCP28 nucleotide sequence (kbp12):

aatttgctttatctttgcattgttgttggc**atggctotcaatctccgtc**agaaaacagactgaatg
tgtaatccggatgttgaatctgaaccaacctttgaatccaagtggaaactgcgaacgaagaagttt
acaagatcttgatttacgataggttttgtcagaacattctatctccattgacccatgtcaaggat
ctgcgtaagcatggagttacactcttctttctcatagacaaagatcgacaacctgttcatgatgt
tcccgtgtctactttgttcaaccaactgaatccaacctccagaggatcatagccgatgcttcta
gatctctctacgataacctttcatctgaatttctcgtcttcgatccctcgtaagtttcttgaagag
ctagcttctgggactcttaaactctggttctgttgagaaagtctcgaaagtgcattgatcagtatct
ggagtttgtgactttggaagataaacttgttctcgtctggctcagcaatctacctatgttcaaataga
atgacccatcagcaggggagaaagagattaatgagattatcgaaagggtcgctagtgggttgtt
tgtgtgttggtaacgcttgggtgtggttctgttatccgatgccctagtgggtggacctgcagagat
gggtggcgtcttgggtgagcagaaactgagggatcatctttgtccaagaacaatctgtttactg
aagggtggcggtttcatgagctcgtttcagcgtccctcttgtgcataatttgataggaactttgag
ctctcgggttgggattcagcatgatttcagataccggcctctcgttcacgatgttctcgggttaa
gctcaaccaattgaaagtgcagggagagaaaggaccaccgaaatcgtttgagctggacagttcgg
acctattctggtcagcaaacagtactctggagtttccagatgtcgtctgtggagatcgaaacacag
ttgaacaagtacaagagagacgttgaagaggttaacaagaaaaccggaggtgggagcggcgctga
gtttgatgggacagatctgattggaaacatccacaccgagcatctcatgaacactgtgaaatcgc
tcccggagttaactgagcgaagaaagtgattgacaaacacaccaatatcgcaacagcgctctta
ggacagatcaaggagagatctattgacgctttcactaagaaagaaagcgacatgatgatgagggg
cggaatcgacagaactgaacttatggctgctctgaaaggcaaagggacaaagatggacaagctcc
ggtttgcaatcatgtacctgatctccacagaaaccataaaccaatcggaagttgaagcagtggag
gcagcattgaatgaagctgaggctgatacaagtgcgtttcagtatgtaaagaaaatcaaatacgtt
aaacgcatcttttgcagctacatcagcgaattcagctagcagaagcaacattgtagactgggccc
agaagctttacggacagtctataagcgcagtgactgcaggagtcaagaatctgttatctagtgat
caacaattggcagtgactcgaacagtcgaagctttaacagaaggaaaaccaaaccggagatcga
ttcttaccgcttcctggacccaagagctccaaagtcgtctagctccggtggtagccatgtaaaag
gaccgttcagagaagctatagtgttcatgatcgggtggaggttaactatgttgagtatggaagtttg
caggagttgactcagagacagtttaaccgttaaaaaacgttatattatggagccactgagattcttaa
cggaggtgagttgggtggagcagcttggacttttgggaaagaagatgggattaggaggtccggctcg
cttcaacgctgaagaggtggtggaatggctggttaaagaggagactgatgtatctgcacaagggtct
ttaaccagggaggccactgagatatggaggagtgagttggaatctcgccgggttccaggtagatag

FIGURE 32

34/65

tttagaagctgaacttgttggtgtcgaaggtctaccttgagtttgctcagaagaagagatgccagaa
aggagttaggagtctcttgcgggtagggtcagatcgactcgcaactatgtttgcgttattttgagatca
aaagctagagttctggccatttcctgatgatctagcaaatgtgtcatgcggtgtggaacagattga
agaactgaaaggattgaaccttgttgagaaagatggtggttcattcttcttgacggggctagga
acactaatcctgaaactagaaggtagagtggttccttgggtgttagaggatggagcctataactaat
gagatgctccagtcctatagagatggttactgatgtgctggactctcttgtgaggagggttacagt
agcagaatctgagttctgctgttcaaaaggagagggcacttttgggagaggaa-gaaatcagtagg
- in KBP12 a in KBP12
aa-gactatccaaatcgaaaatttgtccgtgaagttagaagagatggaacgatttgccttatggga
a in KBP12
ctaatagtgttctaaacgaaatgcgggaaaggattgaggaattagttgaagagacgatgaggcag
agggaaaaagctgtggaaaacgaagaggagttgtgtcgtgtgaagagagagattcagagtcgcttaa
in KBP12 n nn n
aagctacgtcagtaacttttaccaatgttcgagaaacacttctttcgtccgagagacaattcaaaa
ccattgaggagctctttgaacggttggtcactaagacgacacaattagaaggggagaaggcaca
aaggaggttgaagtacagaaactgatggaggagaatgtgaaattgacagcacttctcgacaagaa
agaggctcagcttctagctttgaatgaacaatgcaaagttatggctttgagtgcatcaaacata
gactctctaataccaaccgaatctcaagcttc

FIGURE 32 (continued)

35/65

CCP molecule: CCP28 amino acid sequence (kbp12):

MALNLRQKQTECVIRMLNLNQPLNPSGTANEEVYKILIYDRFCQNILSPLTHVKDLRKHGVTLFF
LIDKDRQPVHDPVAVYFVQPTESNLQRIIADASRSLYDTFHLNFSSSI PRKFLEELASGTLKSGS
VEKVSKVHDQYLEFVTLEDNLFSLAQQSTYVQMNDP SAGEKEINEI IERVASGLFCVLVTLGVVP
VIRCPSGGPAEMVASLLDQKLRDHLLSKNNLFTEGGGFMSSSFQRPLLCIFDRNFELSVGIQHDFR
YRPLVHDVLGLKLNQLKVQGEKGPPKSFELDSSDPFWSANSTLEFPDVAVEIETQLNKYKRDVEE
VNKKTGGGSGAEFDGTDLIGNIHTEHLMNTVKSLPELTERKKVIDKHTNIATALLGQIKERSIDA
FTKKESDMMMRGGIDRTELMAALKGKGTKMDKLRFAIMYLISTETINQSEVEAVEAALNEAEADT
SAFQYVKKIKSLNASFAATSANSASRSNIVDWAEKLYGQSI SAVTAGVKNLLSSDQQLAVTRTVE
ALTEGKPNPEIDSYRFLDPRAPKSSSSGGSHVKGPFREAI VFMIGGGNYVEYGSLQELTQRQLTV
KNVIYGATEILNGGELVEQLGLLGKKMGLGGPVASTLKRLGMAGKEETDVSAQGS LTREATEIWR
SELESRRFQVDSLEAELVDVKAYLEFGSEEDARKELGVLSGRVRSTATMLRYLRSKARVLAI PDD
LANVSCGVEQIEELKGLNLVEKDGGSSSSSDGARNTNPETRRYSGSLGVEDGAYTNEMLOS IEMVT
DVLDSLVRRTVAESES AVQKERALLGEEETSRKTIQIENLSVKLEEMERFAYGTNSVLNEMRER
IEELVEETMRQREKAVENEEELCRVKREFESLKS YVSTFTNVRETLSSERQFKTIEELFERLVT
KTTQLEGEKAQKEVEVQKLMEENVKLTALLDKKEAQLLALNEQCKVMALSASNI

FIGURE 33

36/65

A.

CCP molecule: CCP29 nucleotide sequence (kbp13):

ATGACCAATATCGCCATGGCTGATGCTCTCAAATCTCTTGAGATTGTTGATGGTCTTGATGAATA
CATGAATCAATCTGAATCCAGTGCTCCGCATTCTCCAACCAGTGTAGCAAAGCTGCCACCAAGCA
CTGCAACTAGAACAACTCGACGGAAGACCACAACAAAAGCTGAGCCTCAGCCATCATCTCAGTTG
GTGTCCCGTTCTTGTCTGTTGACGAGCAAGTCTCTTGCTGGAGATATGGACCAGGAAAACATAAA
CAAGAATGTTGCTCAAGAAATGAAGACTAGCAATGTCAAGTTTGAAGCCAATGTGCTCAAACTC
CAGCAGCAGGAAGCACAAAGGAAAACCTTCAGCAGCAACTTCTTGCACTAAGAAGGATGAATTGGTC
CAGTCGGTCTACAGCACTAGGAGATCAACCAGGCTGTTAGAGAAATGTATGGCCGATCTGAGTTT
GAAGACTAAAGAACTGTGGATAATAAACCTGCCAAGAATGAAGATACAGAACAGAAAGTATCTG
CACAGGAGAAGAATCTAACTGGTTAG

B.

CCP molecule: CCP29 amino acid sequence (kbp13):

MTNIAMADALKSLEIVDGLDEYMNQSESSAPHSPTSVAKLPPSTATRTRRKTTHKAEPQPSSQL
VSRSCRSTSKSLAGDMDQENINKNVAQEMKTSNVKFEANVLKTPAAGSTRKTSAAATSCCKDELV
QSVYSTRRSTRLLKCMADLSLKTKETVDNKPKNEDTEQKVSAQEKNLTG

FIGURE 34

37/65

A.

CCP molecule: CCP30 nucleotide sequence (kbp15):

atgctgatgctgtgtgggttcacgggtcttggatatgctaaagcaccacgaccttgggaagatccg
 agcacccttgcacccctctcagaaagaagatgcagattcagcacgcttaccagcagatacatcagg
 ggtcaaaactgttgaagatggaccggatgatgttgagagggaccaaaaaagaaggatagcgctgag
 gaaaggaaacctgcaaagagagagaaggaagaaagacatgataggcgtgaaaaacgcgaaaggca
 tgagaagcgaagcgctcgtgattcagatgatagaaagaagcacaagaaagagaagaaggagaaaa
 aaagaaggcatgactctgattctgattgaagcgaattgtcccaggatggaacattttgctcttca
 gaggaagagtggcggttaggtaccaaaatccagctaccacttctgcaagatttaaactctgttgc
 ttatttcatttacgaatcgtggagtaaagtgtgtgtga

B.

CCP molecule: CCP30 nucleotide sequence (kbp15):

ggctgataaatatagggagaactatttgggtcacagtatcaaagccctgttgggaagatggcaaa
 aaggtaaagatcttcatttgggtatgctagagataaaaagcaaaaggggtccgagatggatgctatg
 aaagaagagattcaaagagttaaggaacaagaggagcaggccatgaggaggctcttggcttggc
 accaaagtcctctacaaggccacaaggaaatcgcccttgataagcaagagtttactgaacttgtga
 agaggggttcgacagcagaggacttaggtgcagggaatgctgatgctgtgtgtgggttcacgggtctt
 ggatatgctaaagcaccacgaccttgggaagatccgagcacccttgcacccctctcagaaagaaga
 tgcagattcagcacgcttaccagcagatacatcaggggtcaaaactgttgaagatggaccggatg
 atgttgagagggaccaaagaaggataggcgtgaggaaggaacctgcaaagagagagaaggaag
 aaagacatgataggcgtgaaaaacgcgaaaggcatgagaagcgaagcgctcgtgattcagatgat
 agaaagaagcacaagaagaagaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaag
 cgaattgtcccaggatggaacattttgctcttcagaggaagagtggctcggttaggtaccaaaatc
 cagctaccacttctgcaagatttaaactctgttggcttatttcatttacgaatcgtggagtaaagtg
 ttgttgaacattgttggaaaatgtttgttaaaacacatgaaaaatgtgggttgatattatacaaaa
 ccgagacgctcgtttttagct

C.

CCP molecule: CCP30 amino acid sequence (kbp15):

MLMLCGFTVLDMLKHHDLGKIRAPLHPLRKKMQIQHAYQQIHQGSKLLKMDRMMLRGTRRRIGVR
 IGNLHRESRKEDMIGVKNAGMRSEALVIQMIERSTRKRRRRKKEGMTLILIEANCPRMEHFALQ
 RKSGRLGTKIQLPLLQDLNLLISFTNRGVKCC

D.

CCP molecule: CCP30 amino acid sequence (kbp15):

MDAMKEEIQRVKEQEEQAMREALGLAPKSSTRPQGNRLDKQEFTELVKRGSTAEDLGAGNADAVW
 VHGLGYAKAPRPWEDPSTLASSQKEDADSARLPADTSGVKTVEDGPDDVERDQRRIGVRKGNLQR
 ERRKKDMIGVKNAGMRSEALVIQMIERSTRKRRRRKKEGMTLILIEANCPRMEHFALQKSGRL
 GTKIQLPLLQDLNLLISFTNRGVKCC

FIGURE 35

38/65

CCP molecule: CCP31 nucleotide sequence (kbp20):

GCAAAAGAGAGAAACATCTGACCCGGAATCTGACCTGAAAACCCGGAAGAATCGAAAAATG GGGGA
AAGATGGTCTGAGCGACGATCAGGTCTCGTCGATGAAGGAAGCCTTCATGCTCTTCGACACCGAT
GGCGACGGCAAAATCGCACCGTCAGAGCTCGGGATCCTCATGCGATCTCTCGGCGGAAACCCGAC
CCAAGCCCAGCTGAAATCCATAATCGCATCCGAGAATCTCTCTTCACCGTTTGATTTCAACAGAT
TCCTCGATCTCATGGCGAAACATCTGAAGACGGAACCTTTTCGATCGCCAGCTCCGTGACGCATTC
AAAGTGCTCGATAAGGAAGGTACCGGGTTCGTTGCTGTGGCGGATCTGAGGCATATTCTGACCAG
TATCGGAGAGAAGCTGGAGCCTAATGAGTTCGATGAGTGGATCAAGGAGGTGGATGTTGGATCCG
ATGGAAAGATCCGGTATGAAGATTTTCATAGCAAGGATGGTTGCTAAGTGA GATCTAATCTTTTAT
GTTTTGAAAGTTGAAATTTTTTAAGAAGAGATTCTTTTGNGGTTTTTTTCACTTGGTTGGTTTGATT
TCGAGCGAATCCTAACTAGGGGTTGGTTTATCATTGNGGAATTTGCTTACTAACTTTGGCTTCTT
CATGGTTGGGTTTCAATTTTTTAATGGNAAATGGTGGCTGGGGGAATTCCTAAAAAAAAAAAAAAAA
AAAAAAA

FIGURE 36

39/65

CCP molecule: CCP31 amino acid sequence (kbp20):

MGKDGLSDDQVSSMKEAFMLFDTDGDGKIAPSELGILMRSLGGNPTQAQLKSIIASENLSSPFDF
NRFLDLMAKHLKTEPFDRQLRDAFKVLDKEGTGFVAVADLRHILTSIGEKLEPNFDEWIKVDV
GSDGKIRYEDFIARMVAK

FIGURE 37

40/65

A.

CCP molecule: CCP32 nucleotide sequence (E2F5BBC16):

caaaaaaagagatcgcttcagtcgagaaaacagagtgactcaaccaatttgcggccaaagaggctctc
caacttctcaattgcgtcgcgggagtctcctttcgatcaagagaaatgcgtccgatttttgcaatc
tctcagagaatgcgttctatcaaagaaagtaaagaagttctcgataccgagtcagatcacgact
ctgagggagcagcttcagctacaaagagaccttcacaacgttctttgttccgattttcttttatac
gtttgagttgtaatcatgtaattgattttaatgtcatgccttggattcataagctgggtcatgcc
ttgtttcccctttgttgtcttgtatgttgaatattgcaaactctaaagagcatatttataagaag
aaataaaagtttctacaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP32 amino acid sequence (E2F5BBC16): SEQ ID NO:126

MEKQSTQPICGQEALQLLNCVAESPFDQEKCVRFLLQSLRECVLSKKVKKFSIPSQDHDSEGAASA
TKRPS

C.

CCP molecule: CCP32 amino acid sequence (E2F5BBC16): SEQ ID NO:98

RGVSFRSREMRPIFAISQRMRSIKESKEVLDTESRSRL

FIGURE 38

41/65

A.

CCP molecule: CCP33 nucleotide sequence (DP):

atgacaactactgggtctaattctaatcacaaccaccatgaaagcaataataacaacaataaacc
 tagtactaggtcttggggcacggcggtttcagggtcaatctgtgtctactagcggcagtatgggct
 ctccgtcgagccggagtgagcaaaccatcaccggttggtacatctactagcgacactacttttcaa
 cgcctgaataattggacattcaagggtgatgatgctggttctcaaggagcttctggtgtaagaa
 gaagaagaggggacagcgtgcggtggtccagataagactggaagaggactacgtcaatttagta
 tgaaagtttgtgaaaagggtggaagcaaaggaaggacaacttacaatgaggttgacagcagcgtt
 gttgctgaatttgcacttccaaataacgatggaacatccctgatcagcaacagtatgatgagaa
 aaacataagacgaagagtatatgatgctttaaacgtcctcatggctatggatataatatccaagg
 ataaaaaagaaattcaatggagaggtcttctcggacaagcttaagcgacattgaagaattaaag
 aacgaacgactctcacttaggaacagaattgagaagaaaactgcatattccaagaactggaaga
 acaatatgtaggccttcagaatctgatacagagaaatgagcacttatatagctcaggaaatgctc
 ccagtggcggtgttgctcttcttttatccttgtccagactcgtcctcacgcaacagtagaagt
 gagatatcagaagatatgcagctcgtgcattttgatttcaacagcactccatttgagctccacga
 cgacaattttgtcctcaagactatgaagttttgtgatcaaccgcccgaacaaccaaacggtcgga
 acaacagccagctggtttgtcacaatttcacgccagaaaaccctaacaaggccccagcacaggt
 ccaacaccgcagctggaatgtacgagactcatcttcaatcgcaacaacatcagcagcattctca
 gctacaaatcattcctatgcctgagactaacaacgttacttccagcgtgatactgctccagtga
 aatccccgtctcttccagggataatgaactccagcatgaagccggagaattga

B.

CCP molecule: CCP33 amino acid sequence (DP):

MTTTGSNSNHNHESNNNNNNPSTRSWGTA VSGQSVSTSGSMGSPSSRSEQTITVVTSTSDTTFQ
 RLNNLDIQDDAGSQGASGVKKKKRGQRAAGPDKT**GRGLRQFSMKVCEKVESKGRTTYNEVADEL**
VAEEALPNNDGTSPDQQQY**DEKNIRRRVYDALNVL****MAMDIISKDKKEIQWRGLPRTSLSDIEELK**
 NERLSLRNRIEKKTAYSQELEEQYVGLQNLIQRNEHLYSSGNAPSGGVAL**PFILVOTRPHATVEV**
EISEDMOLVHFDENST**PFELHDDNFVLKTM**KFCDPQPQPNGRNNSQLVCHNFTPENPNKGPSTG
 PTPQLDMYETHLQSQHQHSQLQIIPMPETNNVTSSADTAPVKSPSLPGIMNSSMKPEN

FIGURE 39

42/65

A.

CCP molecule: CCP35 nucleotide sequence

atggcgctgcagaacattgggtgcttccaaccgtaacgatgccttctacaggtacaagatgcctaa
 gatggttaccaaaaccgaaggcaaaggtaatggcattaagaccaacattatcaacaatggtgaga
 ttgccaaagccttggctagaccgccttcttatacgaccaagtaactttggttgtagcttgagcg
 cagtctaagtttgatgagaagactgggacgtcgcttgatgaatggagctcacaacacgtctaagct
 tgctgggcttttgagaattttattaagaagtttggttcagtggttatggatgtggttaaccggaga
 ctgagattattattacgaagacgcagatgggtgaatctcaagtggtgctgcttggtgggtttatctct
 gaggtcgacatgagggataagttgactaatttcattctcaagaaccacctgagcagaagaaggt
 gtcaaaggataagaaagcaatgaggaaagctgagaaggagaggcttaaagaaggcgagctagctg
 atgaggagcagagaaagctgaaagctaagaagaaagcattgtctaacggcaaggattctaagacg
 tctaagaaccattcttctgatgaggatataagcccgaaagcatgatgagaatgctctagaggtgga
 tgaggatgaagatgatgatgatggtgtcgagtggcaaaactgatacttcccagagaagctgctgaga
 aaagaatgatggaacagttgagtgctaaaactgcccgaatggtgatgctctctgcaatggaagta
 gaagagaaaaaggcgcccaaaagcaaatctaacgggaacggtgtgaaaactgagaatcctcctcc
 gcaagagaagaatctcgtgcaggatatgaaagagtatctgaagaaagggtcaccaataagcgcg
tcaaaggtttcatctcgtctctctctgaacctcctcaagacatcatggacgcactcttcaatgct
ctctttgatgggtgtgggaaagggttcgccaaagaagtgactaagaagaagaattacttagcggc
tgctgcaacaatgcaagaggatggatcacagatgcactctgctcaattcgattgggacattctgtg
gaaagaatggaaacgaagaagccttgaaagaggtggctctggttcttaaagcattgtacgaccaa
gacatcattgaggaagaggtagtgttgattgggtacgaaaagggtctcaccggagctgacaaaag
ctcgccggtttggaagaatgttaagccttttgtggagtggcttcagagcgctgagctctgagtcg
aagaggaggattgagtcacttttttctccctcctaacttttcttttgcggcatttcttataatac
ttcgtcagttttcagaattcttaaatcttttgcgtgtgttcttataaagaacatcatctattaa
agttgtcttcgttttggttttgacgactttgggaaatatattatgtttaagaaaaaaaaa
aaaaaaaaaaaa

B.

CCP molecule: CCP35 amino acid sequence

MALQNIGASNRNDAFYRYKMPKMTKTEGKGNGIKTNIINNVEIAKALARPPSYTTKYFGCELGA
 QSKFDEKTGTSLVNGAHNTSKLAGLLENFIKKFVQCYGCGNPETEIITKTQMVNLKCAACGFIS
 EVDMRDKLTNFI LKNPPEQKKVSKDKKAMRKAERLKEGELADEEQRLKAKKKALSNGKDSKT
 SKNHSSDEDISPKHDENALEVDEDEDDDDGVEWQTDTSREAAEKRMMEQLSAKTAEMVMLSAMEV
 EEKKAPKSKSNGNVVKTENPPPQEKNLVQDMKEYLKKGSPI SALKSFISLSEPPQDIMDALFNA
 LFDGVGKGFAKEVTKKKNYLAAAATMQEDGSQMHLINSIGTFCKNGNEEALKEVALVLKALYDQ
DIIEEEVVL DWYEKGLTGADKSSPVWKNVKPFVEWLQSAESESEED

FIGURE 40

43/65

CCP molecule: CCP36 nucleotide sequence

atggcgggctaacaattcgcgactctgattcatcggaacaaacgaatcactttaatcctcgt
 atacgcttttctcgaatggtcactcattttcttcattttgctcaactctctcttttcttatttca
 tactcagattcgcgtgattatttcgggtcttaaacgctccttgtctcttctgctctagactcgcgt
 ttcttcgatgcttctggtaaatctccttctcatcgagatccttctctgcatgatcatgctctcca
 attacattcaaaacctggttgaagaatctaattgtgggttcggagaatttcacaatgatttggttc
 atcgtggttggtgctgtagagaagataagttcgtcactatgtgctccgattgagtctgactttggg
 aatttagattatccaattggagatgaagggtcagatttacaatgggtcttaagtttcctcgatcgat
 cttcgtctttgaagaagagaaagtaggatctgtaaatgtgaatgattctcaggaagaaacagagg
 agaagaaagttccccaatctcatgagaaacttgaagatgatgatggtgatgaggagttttcatgc
 tatgtatcaagcttcgattgtaagaacaaagaaattgcaacagagaaggaagaagaaaacagagt
 ggatctacctatagagggtgaaactgcagaatcagctccgaaaaacctcgagttctatatattgatg
 aagaagactgtcatttgattccagttgaattctataaacaggagtgaagaagttcgagagatttcc
 gacattaacggagattttatcctcgatttcggcgttgagcatgatttcacggcggcggcgggagac
 ggaggaaatctccgactttgcttcgccgggtgaatcgaaaccggaggatgcagagacgaatctag
 ttgcttcggaaatggaaaacgacgacgaagaaacagacgcagagggtttctataggtacagagatt
 cctgatcatgagcaaactcgagatattccttctcaccagctcattcctcaccacgatgacgatga
 tcatgaggaggaaacggttgaggttcaaaacagtaacgattgaaaccaagatgccagttctaaaca
 tcaacgaagagcggattttagaagctcaaggctcgatggaaagctcgcatagtagtctacataac
 gctatgtttcacttagagcaaagagtatctgttgatggtattgaatgtcctgaaggagtactcac
 tgttgataagttgaagtttgagttacaagaagagagaaaaagcattcacgcgttatacgaggagc
tggaggtagagaggaatgcgtctgctgttgctgccagtgaaacaatggcgatgatcaataggttg
catgaggagaaagctgcgatgcagatggaagcgttgcagttatcagagaatgatggaggagcaagc
tgagtttgatcaagaagctttgcagttggttgaatgagccttatggtgaatagagagaaggagaatg
ctgagcttgagaaggagctagaggtgtatagaaagagaatggaggagtagaagcctaagagaaa
atggggatgttgaggaggagattgagagattcctcgttgattcgtatagaaataatggcgattc
tgatgagaatagcaatggagagttacagtttaagaacggtgaaggggttacggattggaaatata
gagagaatgagatggagaatacgccgggtggatgttgtacttcgtcttgatgagtggttagatgat
tatgatggagagaggctttcgattcttgggagattgaagtttcttgaagagaaactcacagatct
taataacgaagaggacgacgaggaggaggctaaacgtttgagagtaatggtagcatcaatggaa
atgagcatattcatggcaaagaaacaaacgggaagcacagagttatcaagtcaaagagatta
 in E2F3ca2: c a
 cttcccctgtttgatgcggtcgatggagagatggaaaacgggttaagtaacggaaaccatcacga
 aaacgggtttgatgattcggagaagggtgagaatgtgacgatagaagaagaagtggatgagcttt
 acgagaggttagaagctctagaggcagatagagagttcttaagacattgtgttggttcattgaaa
 aaaggagacaaaggtgtacatctcctccatgagattctgcaacatcttcgtgatctaaggaatat
 cgatcttactcgcgtcagagaaaaacggagacatgagtttatgagtttgattttgagttttgggtt
 tgagtccactctttgcatagtgacccaaagaacaagaaaaatcatacaggtatggaagtgcacatg
 ttgctt**gtgaggcaaggaacaacgaca**agggtttcagatgaagaagaaaaacggttctcagaataaaa
 gtattttaagtataactctgaggaaaagtgtcagatcagaatgttcgtctttcttcgttcattt
 tcattattataagttttgttttttatattgaagattttatttagagagaggggaagtgtcagtataa
 tttcacttttatatttttatatttgggagttgtctttatgagtggtggttaataaaaaaggtagaa
 tgatgagtgaagaaaaaaaaaaaaaaaaaaaaa

FIGURE 41

44/65

CCP molecule: CCP36 amino acid sequence

MAANKFATLIHRKTNRITLILVYAFLEWSLIFFILLNSLFSYFILRFADYFGLKRPCLFCSRLDRFFDASG
KSPSHRDLLCDDHALQLHSKPVEESNCGFGEFHNDLVHRGCCVEKISSSLCAPIESDFGNLDYPIGDEGQI
YNGLKFRRSIFVFEEEKVGSVNLNDSQEETEEKVPQSHEKLEDDDDVDEEFSCYVSSFDCKNKEIATEKEE
ENRVDLPPIEVETAESAPKNLEFYIDEEDCHLIPVEFYKPSSEEVREISDINGDFILDFGVEHDFATAAETEE
ISDFASPGESKPEDAETNLVASEMENDDEETDAEVSIGTEIPDHEQIGDIPSHQLIPHHDDDDHEEETLEF
KTVTIETKMPVLNINEERILEAQGSMESSHSSLHNAMFHLEQRVSDGIECPEGVLTVDKLFELQEERKA
LHALYEELEVERNASAVAASETMA MINRLHEEKAAMQMEALQYORMMEEQAEFDQEALQLLNELMVNREKE
NAELEKELEVYRKRMEEYEAKEKMGLRRRLRDSSVDSYRNNGSDENSNGELQFKNVEGVTDWKYRENEM
ENTPVDVVLRLDECLDDYDGERLSILGRLKFLEEKLTDLNNEEDDEEEAKTFESNGSINGNEHGHGKETNG
KHRVIKSKRLPLPFDVDAVDGEMENGLSNGNHHENGFDSEKGENVTIEEEVDELYERLEALEADREFLRHCV
GSLKKGDKGVHLLHEILQHLRDLRNI DLTRVRENGDMSL

FIGURE 42

45/65

CCP molecule: CCP36 nucleotide sequence

atgtcagacgctctttctgcgattccggcgcgagttcatcgcaatctctccgataaaactctatga
 gaagcgcaaaaatgctgcgcttgagcttgagaatattgtgaagaatctaacttcttcgggtgatc
 atgacaagatctcgaaagtcattgagatggtgattaaggaatttgccaaatctcctcaagcta
 catcggaagggtggtctaattggcttagctgctgtaactgttggtttgtctacagaagctgctca
 atatcttgagcaaatagtgccacctgtgattaattccttttctgatcaagatagccgagttcggg
 actatgcatgtgaagctctctataacattgcaaagggtgtgcgaggcgatttcattattttcttc
 aataagatatattgatgccttatgcaaactctcagcagattctgatgccaatgtccaaagtgtgc
 tcatcttttggatcgcttgttaaggatattgtgacggaaagtgatcagttcagttattgaggaat
 tcataacctcttttaaaagagcgaatgaacgttctcaacccttacgtccggcaatttctggttggg
 tggatcactgttcttgatagtgttccagacattgacatgcttgggttctgccagactttctcga
 tgggttattcaatatgttgagcgactctagtcatgaaatacgacagcaagctgattcagctctt
 cagagtttcttcaagagataaaaaattcaccatctgtagattatggtcgcatgggtgaaatactg
 gtgcagaggggtgcttctcctgatgaattcactcgattaacagccatcacgtgggataaacgagtt
 cgtaaaacttgggggagaccagctcgtgcgttattatgctgacattcttggggctatcttgctt
 gcatacttgacaaagaagagaaaaatcaggggtggttgcctgcgtgaaaccaatgaagaacttcgttca
 atccatgttgaaccctcagatgggtttgatgttggcgcaattctctctgttgcaaggaggcagct
 atcaagtgagtttgaggctactcggattgaagcattgaattggatatcaacacttttaacaagc
 atcgtactgaggtcttgtgcttctgaatgacatatttgacacccttctaaaagcactatctgat
 - in E2F3ca9

tcttctgatgacgtggtgctcttgggttctggaggttcattgctggtgtagcaaaagatccacaaca
ctttcgccagctcatcgattttcttgtccacaatttccgagctgataattctcttttggaaaggc
gcggtgcccttattgtccgaagaatgtgtgtacttttggatgccgaaagagtctaccgagagctc
tctacaattcttgaggagagaataatcttgactttgcttctaccatggttcaggcattgaattt
gattttgcttacttccccggagttatcgaaactgagagaactattaaaagggttactcgtcaatc
gcgaagggaagaacttttgcgttgccttgtatacttcatggtgccattcaccatgg-caattat
 in E2F3ca9 g

aagcctctgcttattagctcaggcttacca-gcatgcgagtgctggtgattcaatcattggtagaa
 in E2F3ca9 a a c c a

gaagacattaacgtc-aaatttct-agtacagcttgataaa-ttgatccggcttctggaaactcc
 c t gc a in E2F3ca9
aatctttacttaccttagattgcagcttctggaaccaggaaggtacacatggttgctgaaaacac
tttatggtcttcttatgttacttcctcagcaaagtgcggcgttcaagatacttaggacaagactc
aaaactgtgccaacgtactcattcagtagtggaaaccaaataggcagagcaacttcaggagttcc
tttctctcagtataagcatcaaaacgaggacggtgacttagaagacgataacatcaacagttctc
accaaggaatcaattttgctgtgcggctacaacagttcgaaaacgtacagaatctacatcgtggc
caggcaaggactagagtgaactactcatatcactcttcttcttcttctacatcaaaggaggtgag
gagatctgaagaacaacaacagcagcagcagcaacaacaacagcaacaacaacaacagcag
caccaccttcttcgacatcatcatcagttgcagataacaatagacctccatcaagaacttcaaga
aaaggccctggtcaattacagctt-taacctacctggtaatcataaataataaataatattccatc

FIGURE 43

46/65

cccgacaatcatcatcttcatcttctttgtgtggacaccaccgatcccttttgtctcctgtaaaa
ttgtatatctctcttttttagtaactcttcaagtttcgacggaacttgtggaaaagctacggtcg
tgccatcatctctttctctctgtcgggttttttttatttacgagagattcttcttcagtcctc
agtctacctttatattgtttttttgggggtttctcgtttctttgaatttgtttcattgtttggag
ctttttataatttttaccttatgtggagatgtaagaaaaagaagtgatcatgtgggttttgtgttgt
ttttttataactggaaaaccacatgagtttgtagaggtcacttattgggatattttatgtcaaatg
atgctcctttttacaaaaaaaaaaaaaaaaaaaa

FIGURE 43 (continued)

47/65**CCP molecule: CCP36 amino acid sequence**

MSDALSAIPAAVHRNLSDKLYEKRKNAALELENIVKNLTSSGDHDKISKVIEMLIKEFAKSPQAN
HRKGGLIGLAAVTVGLSTEAAQYLEQIVPPVINSFSDQDSRVRYACEALYNIKVVVRGDFIIF
NKIFDALCKLSADSDANVQSAHLLDRLVKDIVTESDQFSIEEFIPLLKERMNVLPYVRQFLVG
WITVLDSVPDIDMLGFLPDFLDGLFNMLSDSSHEIRQQADSALSEFLQEIKNSPSVDYGRMAEIL
VQRAASPDEFTRLTAITWINEFVKLGGLVRYADILGAILPCISDKEEKIRVVARETNEELRS
IHVEPSDGFVDGAILSVARRQLSSEFEATRIEALNWISTLLNKHRTVLCLNDIFDTLLKALSD
SSDDVLLVLEVHAGVAKDPQHFRLIVFLVHNFRADNSLLERGALIVRRMCVLLDAERVYRELS
TILEGEDNLDFASTMVQALNLILLTSPELSKLRELLKGSLVNREGKELFVALYTSWCHSPMAIIS
LCLLAQAYQHASVVIQSLVEEDINVKFLVQLDKLIRLLETPIFTYLRQLLEPGRYTWLLKTLYG
LLMLLPQOSA AFKILRTRLKTVPTYSFSTGNQIGRATSGVPFSQYKHQNEGDLEDDNINSSHQ
INFAVRLQQFENVQNLHRGQARTRVNYSYSSSSSSTSKEVRRSEEQQQQQQQQQQQQQQQQRPPP
SSTSSSVADNNRPPSRTSRKGPGQLQL

FIGURE 44

48/65

CCP molecule: CCP37 nucleotide sequence

atgtcactcttgttctcaatccgtccgtttccctccaattcaatccacccaattcctcgtcgtgc
cgccggaatatcctccattcgatgctcaatttctgcaccggagaagaaccgaggaggaggagga
agcagaagcgcgcgacggagctgagaatgacgactcttctgtcttctcggaagtgggtgaagctgtc
tccgctctggagaggagtctccgcctcacttttatggacgagcttatggaacgagctagaaatcg
agatacttcagggtgtttctgaggttatctatgacatgattgctgctgggcttagccctggacctc
gttctttccatggtttggtttagctcacgcgcttaacggcgacgaacaaggcgcgatgcactcg
ctgagaaaaggagctaggtgcaggccaacgtccgcttcctgagactatgattgctttggttcgtct
ctctggttcgaaaagggaatgctacgagaggcctagaaatcctcgccgctatggaaaagcttaagt
atgacattcgtcaagccttggtcattccttgttgaggagctcatgaggatcaatcacttggaagat
gccaataaagttttccttgaagggtgcaagagggtgggatgagagcaacagatcagctttatgattt
gatgattgaagaagattgcaaagctggagatcattctaattgccttagacatctcttacgaaatgg
aggcagctggtagaatggccacaacatttctttcaactgtcttcttagtggtgcaggctacatgt
gggattcccagggtagcttatgctacattcgaaaatatggagtagcgggtgaagggtttatttatgaa
gcctgacactgagacatataactgggtgattcaagcctacactagagccgagtcataatgataggg
ttcaggatgttgctgaattacttggaatgatgggttgaggaccacaaacgtgtgcagccaaatgtg
aagacttatgcgctcttagttgagtgcttcaccaaataattgtgtcgtgaaggagcagattagaca
ttttcgtgctcttaaaaaactttgaaggaggaacagtaattttacacaatgcagggaattttgagg
atcctctctctttgtatctcagggctttgtgtcgcgagaagggaagaattgttgagcttattgatgct
ttagatgcaattgcgcaagataaccaacctaactatacctccaagagccatgattatgagcagaaagta
tcgaacactagtcagctcatggattgaaccattgcaagaagaagctgaacttggctatgagattg
attattttagcgaggtacatagaggaagggggacttactggtgaacgcaagcgttgggtacctcga
agagggaaaactccttttagatcccgatgcttctggttttatataactcaaaccctattgaaacatc
ctttaaacagagatgccttgaagattggaaagttcaccataggaagctcttgagaaccttacaga
gtgaagggtcttccagttctaggagatgcatcagaatctgattacatgagagtggtggagagatta
cggaacataataaaaagggtcctgcactgaatcttttgaagccgaaagcagcaagcaagatgggtgt
atcagagttaaaggaagaactcgaagctcagggtttgccaaattgatggaacaagaaatgtgcttt
accagcgtgtccaaaaagcaaggagaataaacaatctcgaggtcgacctctttgggttcctcca
attgaagaagaagaggaggaggtcgatgaagaagtagacgatttaatatgtcgaatcaagctaca
tgaaggagacacagagttctggaaacgtcggtttcttgagaaggcttgattgaaacttcagttg
aatccaaggaaacgactgaatcagtggttacagggtgaatcggagaaagcgattgaagatatttca
aaagaagctgacaatgaggaggatgatgatgaggaggaacaagaaggagatgaggatgatgatga
aatgaagaggaagaagtggttgttccagaaactgagaatcgagcagaaggagaagatttagtga
agaataaggcagctgacgcgaagaagcatcttcaaattgattggagtccaactcttgaaagaatcc
gatgaagcaaacagaaacaaagaaacgtgggaagagggcatctcgtatgacacttgaggatgatgc
agatgaggatttggttccctgaggaaccatttgaagcattcaaagaaatgagggaaagaaaagtgt
tcgatgtggctgacatgtatacaatagcagacgtttgggggttgacatgggagaaggattttaag
aacaaaactccaaggaaatggtcacaagagtggaagtcgagttggcaattgtgctcatgacaaa
ggtgattgaattgggtggaattccaacgattggtgattgtgcagtgatattacgagctgcttaa
gagctccc

FIGURE 45

49/65

atgccttcagccttcttgaagatcttgcagacgacacacagtcttggctactcatttggcagccc
gttgtagcatgagatcatcacattgtgtttggaccttggagaacttgatgcagccatcgccatag
ttgcagatatggaaaccacagggatcactgtccctgatcaaacccttgacaaggcatatctgct
agacaatctaatagagagtcgcggtctgagcctgaagagccagcatcaacagtaagctcttagtt
atcatacctcttctgcttgttgtgaagtctctataagaaacagaaatcggtagaaggagctgaa
tctgtcttagttatgaaagttttgttcattataagtacaagtcattgtagttccgagtgtagaaca
gtttttactagtgttgaccaggtccctccagtcctgatacttaattctttagtggttgatctttc
tatataagaaaaaaaaaaaaaaaaaaaa

FIGURE 45 (continued)

50/65

CCP molecule: CCP37 amino acid sequence

MSLEELNPPFFRSNSIHPIPRRAAGISSLRCSISAPEKKPRRRRKQKRGDGAENDDSLSEFGSGEAVSALERS
LRRTFMDELMERARNRDTSGVSEVIYDMIAAGLSPGPRSFGHLVVAHALNGDEQGAMHSLRKELGAGQRPL
PETMIALVRLSGSKGNATRGLEILAAMEKLKYDIRQAWLILVEELMRINHLEDANKVFLKGARGGMRATDQ
LYDLMIEEDCKAGDHSNALDISYEMEAAGRMAATTFHFNCLLSVQATCGIPEVAYATFENMEYGEGLFMKPD
TETYNWVIQAYTRAESYDRVQDVAELLGMMVEDHKRVQPNVKTYALLVECFKTKYCVVKEAIRHFRALKNFE
GGTVILHNAGNFEDPLSLYLRLALCREGRIVELIDALDAMRKDNQPIPPRAMMSRKYRTLVSWSWIEPLQEE
AELGYEIDYLARYIEEGGLTGERKRWVPRRGKTPLDPDASGFIYSNPIETSFQRCLEDWKVHHRKLLRTL
QSEGLPVLGDASESDYMRVVERLRNIIKGPALNLLKPKAASKMVVSELKEELEAQGLPIDGTRNVLYQRVQ
KARRINKSRGRPLWVPPIEEEEEVEDEEVDDLICRIKLHEGDTEFWKRRFLGEGLIETSVESKETTESVVT
GESEKAIEDISKEADNEEDDDDEEEQEGDEDDDENEEEEVVVPETENRAEGEDLVKNKAADAKKHLQMIGVQ
LLKESDEANRTKKRGKRASMTLEDDADEDWFPEEPFEAFKEMRERKVFDVADMYTIADVWGWTEKDFKN
KTPRKWSQEWELAIVLMTKVIELGGIPTIGDCAVILRAALRAPMPSAFLKILQTTTHSLGYSFGSPLYDE
IITLCLDLGELDAAIAIVADMETTGITVPDQTLDKVISARQSNESPRSEPEEPASTVSS

FIGURE 46

51/65

A.

CCP molecule: CCP38 amino acid sequence

aagcttcgaagtcgattttcaatggaagggttcctcgtcagccatcgcgaggaagacatgggagcta
gagaacaacattctccagtggaaccaaccgattcagcctccgacagtataattccactacgacga
cgcttcacaagccaaaatccagcaggagaagccatgggcctccgatcctaactacttcaagcgcg
ttcacatctcagcccttgctcttctcaagatgggtgggttcacgctcgctccgggtggcacaatcgag
atcatgggtcttatgcagggtaaaaccgaggggtgatacaatcatcgttatggatgcttttgcttt
gcctgttgaagggtactgagactaggggttaatgctcagtcctgatgcctatgagtatatgggtgaat
actctcagaccagcaagctggctgggaggttgagaaacggttggtggatgggtatcactctcaccct
gggtatggatggttggtctcgggtattgatgtttcgacacagatgcttaaccaacagtatcagga
gccattcttagctgttggtattgatccaacaaggactgtttcggctggtaagggtgagattgggg
cattcagaacatatccagagggacataagatctcggatgatcatgtttctgagtatcagactatc
cctcttaacaagattgaggactttgggtgtacattgcaaacagtaactactcattggacatcactta
tttcaagtcactctctcgatagtcaccttctggatctcctttggaacaagtaactgggtgaacactc
tttcttcttccccactgttgggcaatggagactatgttgccgggcaaatatcagacttggctgag
aagctcgagcaagcggagagtcagctcgctaactcccgggtatggaggaattgcgccagccggtca
ccaaaggaggaaagaggatgagcctcaactcgcggaagataactcgggatagtgcaaagataactg
tcgagcaggtccatggactaatgtcacaggttatcaaagacatcttggttcaattccgctcgtcag
tccaagaagtcctgctgacgactcatcagatccagagcccatgattacatcgtgaagttggtctat
tcttttggttttttggtgctcggaattgactatcggtttgacccggtttatgaggcaatgccatt
gttccctatatctctagtgtagtatctgcttcagacaaagatctttgggttattaaatgacatta
acataaatcgatcattatgttttttgcgttaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

B.

CCP molecule: CCP38 amino acid sequence

MEGSSSAIARKTWELENNILPVEPTDSASDSIFHYDDASQAKIQQEKPWASDPNYFKRVHISALALLKMOV
HARSGGTIEIMGLMQKTEGDTIIVMDAFALPVEGTETRVNAQSDAYEYMVEYSQTSKLAGRLENVVGVYH
SHPGYGCWLSGIDVSTQMLNQOYQEPFLAVVIDPRTVTSAGKVEIGAFTYPEGHKISDDHVSEYQTIPLN
KIEDFGVHCKQYYSLDITYFKSSLDSHLLDLLWNKYWVNTLSSSPLLGNGDYVAGQISDLAEKLEQAESQL
ANSRYGGIAPAGHQRRKEDEPOLAKITRDSAKITVEQVHGLMSQVIKDILFNSARQSKKSADDSSDPEPMI
TS

FIGURE 47

52/65

- + CDC2bDN-IC26M


FIGURE 48

53/65

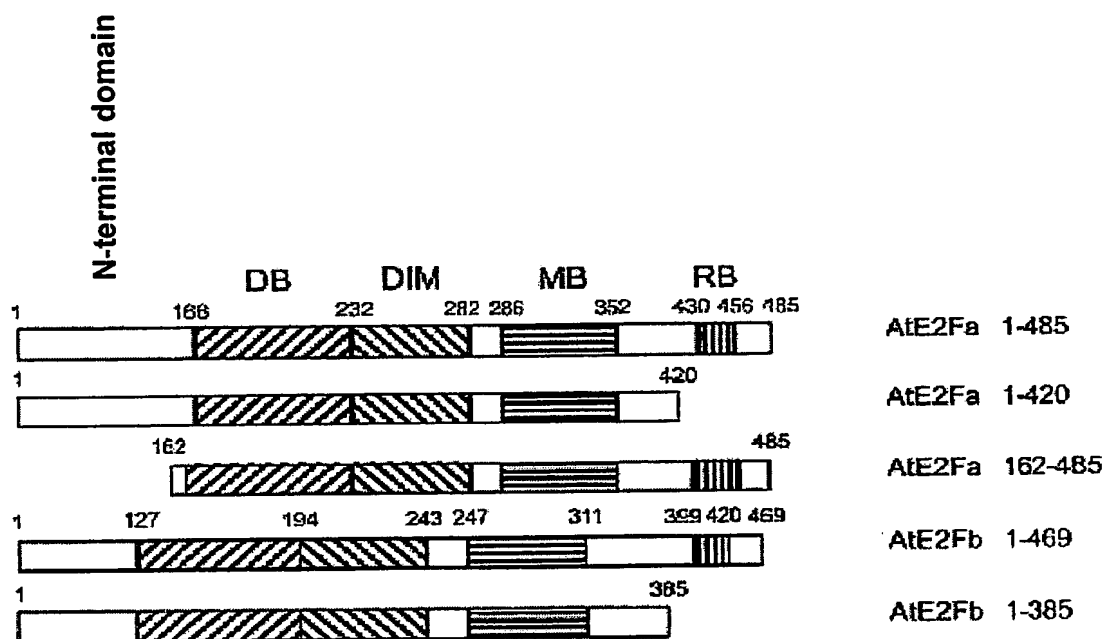


FIGURE 49

54/65

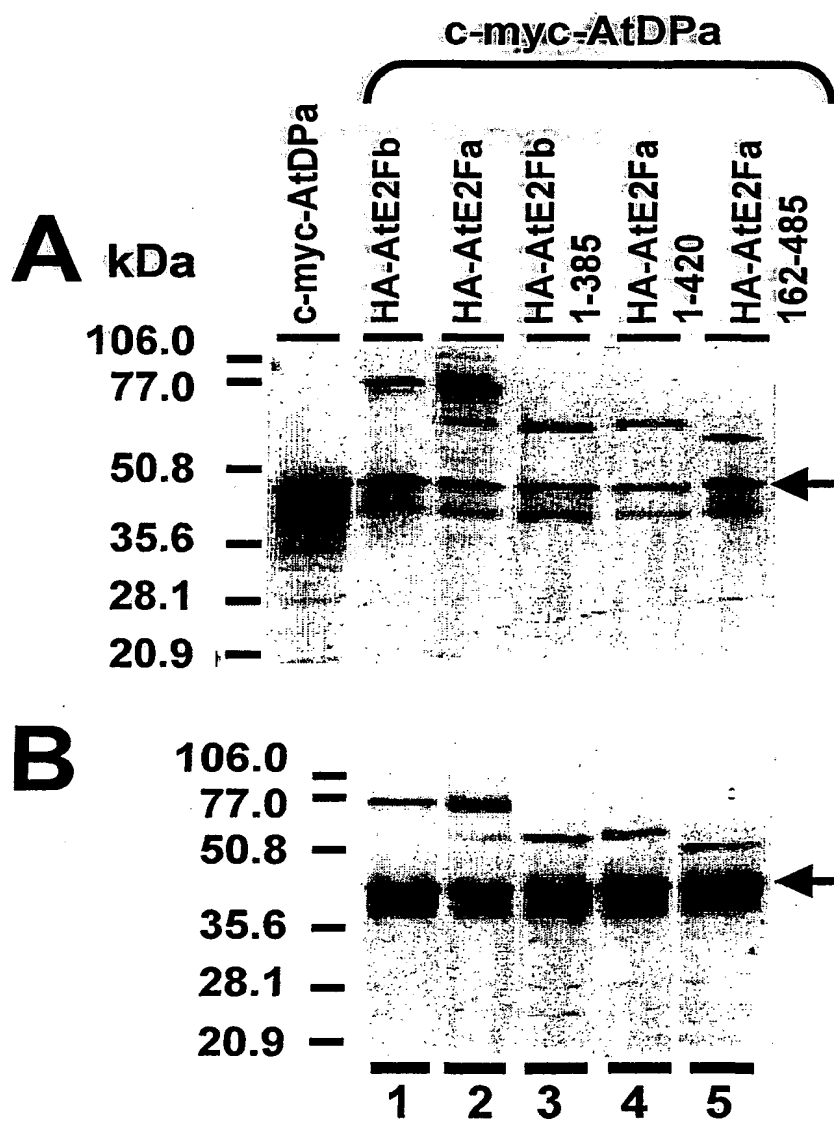


FIGURE 50

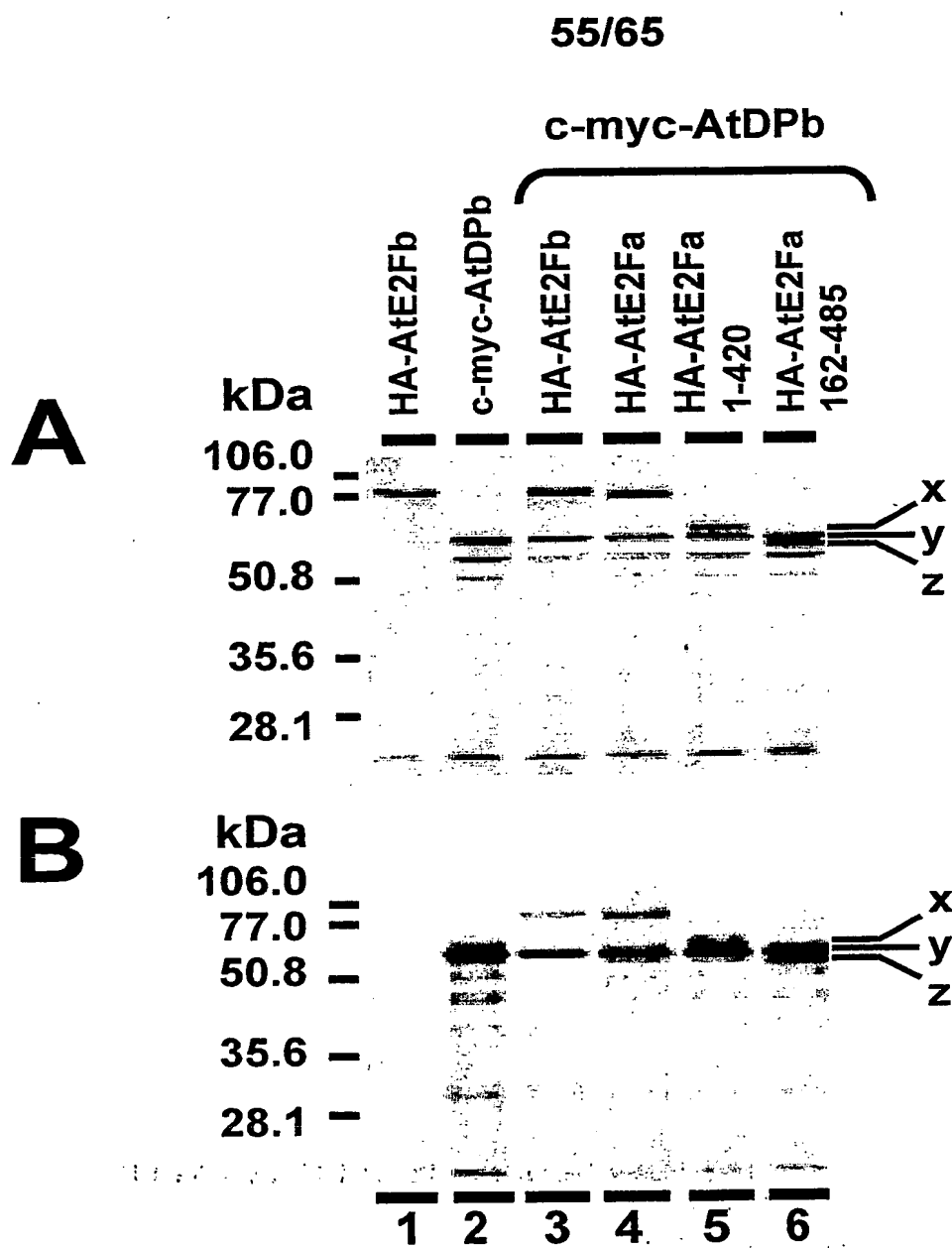


FIGURE 51

56/65

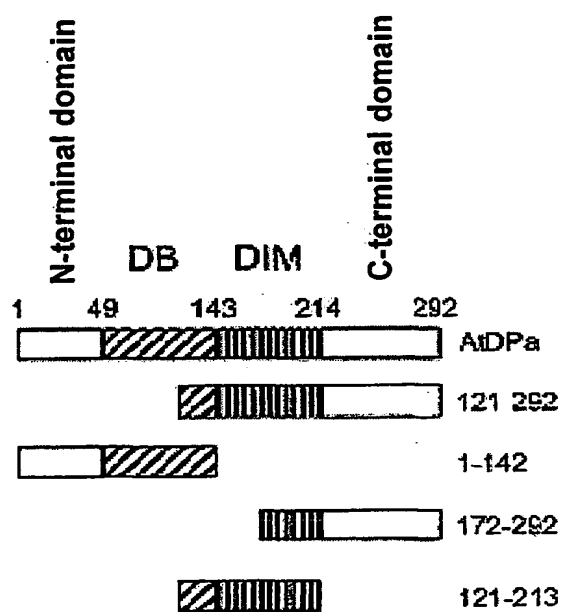


FIGURE 52

57/65

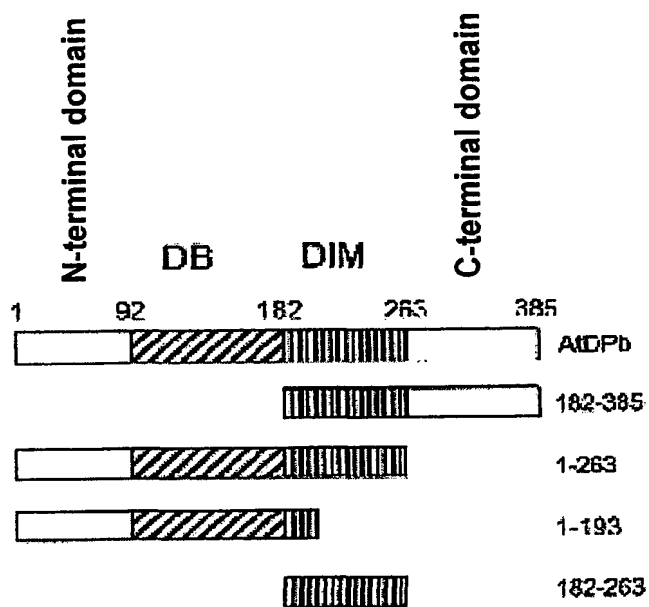


FIGURE 53

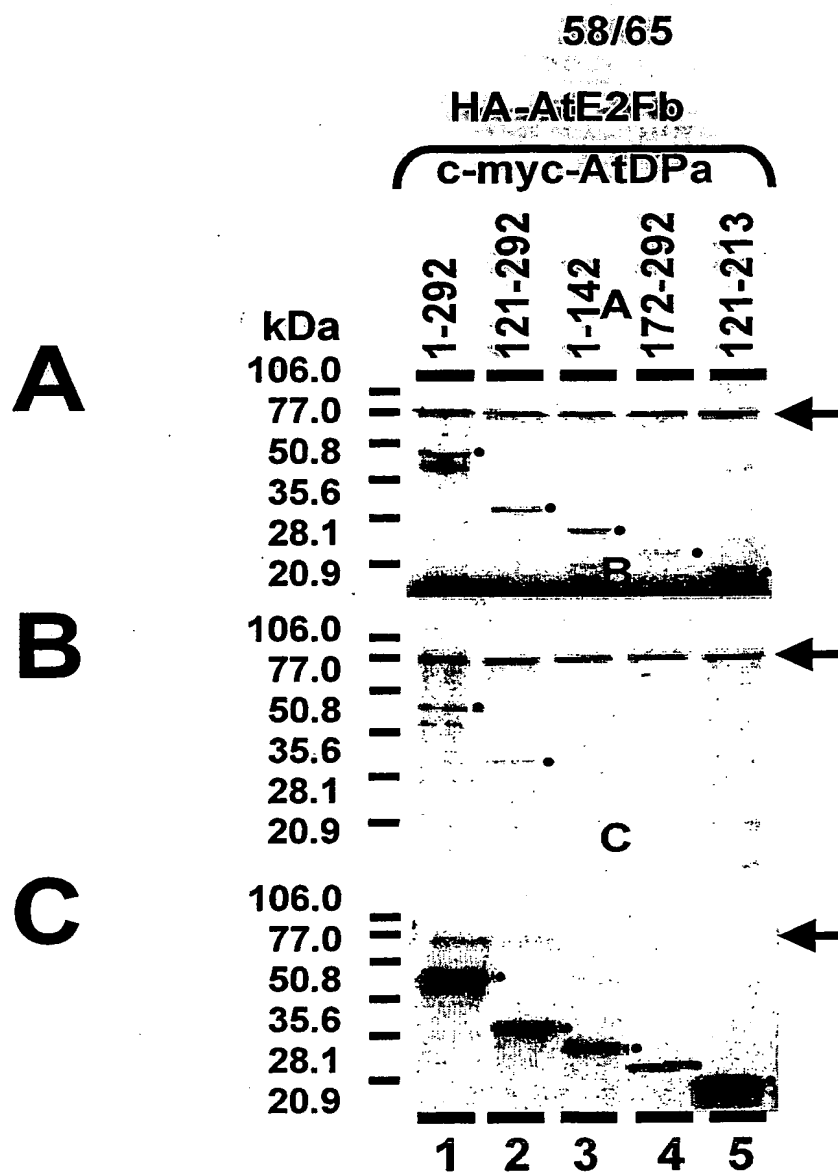


FIGURE 54

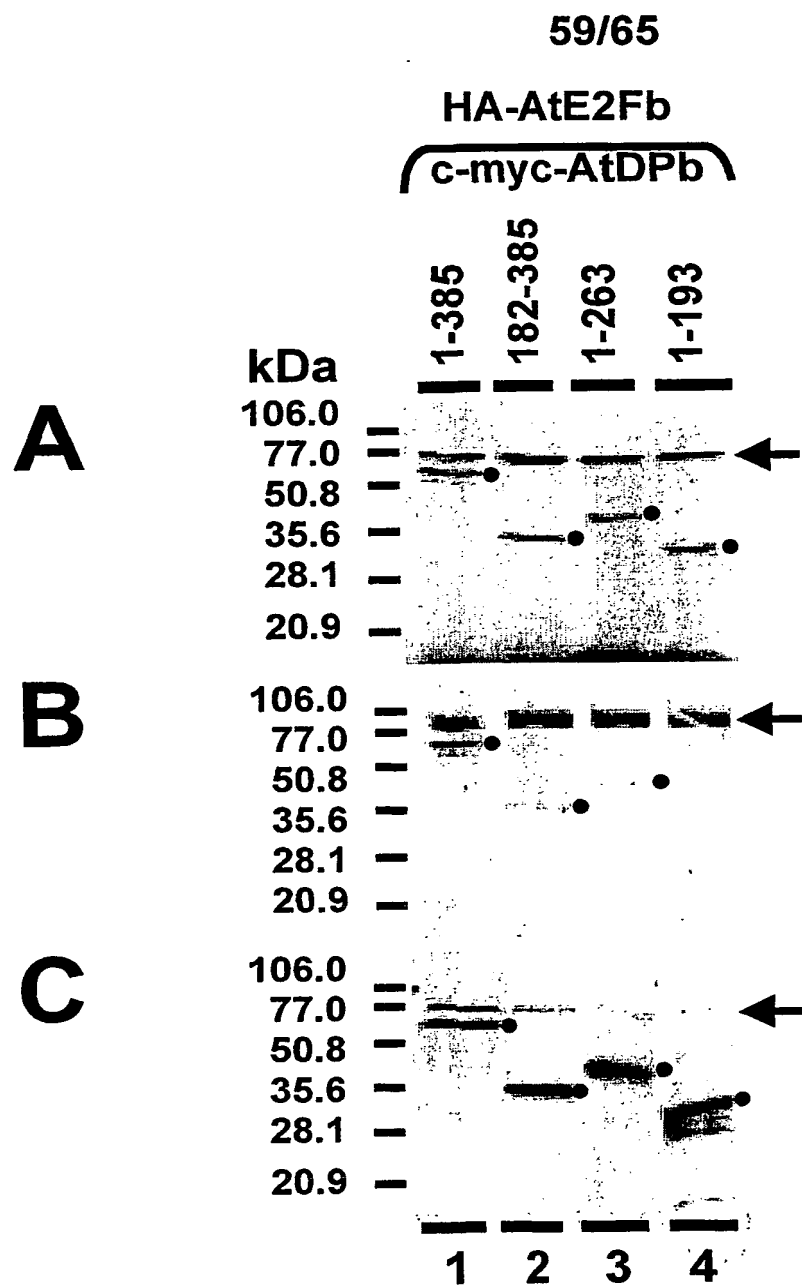


FIGURE 55

60/65

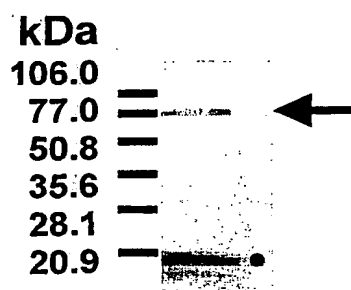


FIGURE 56

61/65

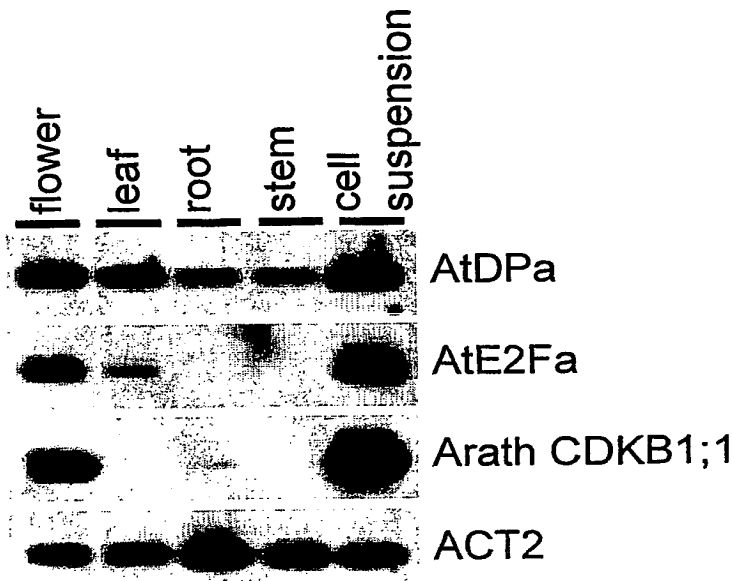


FIGURE 57.

62/65

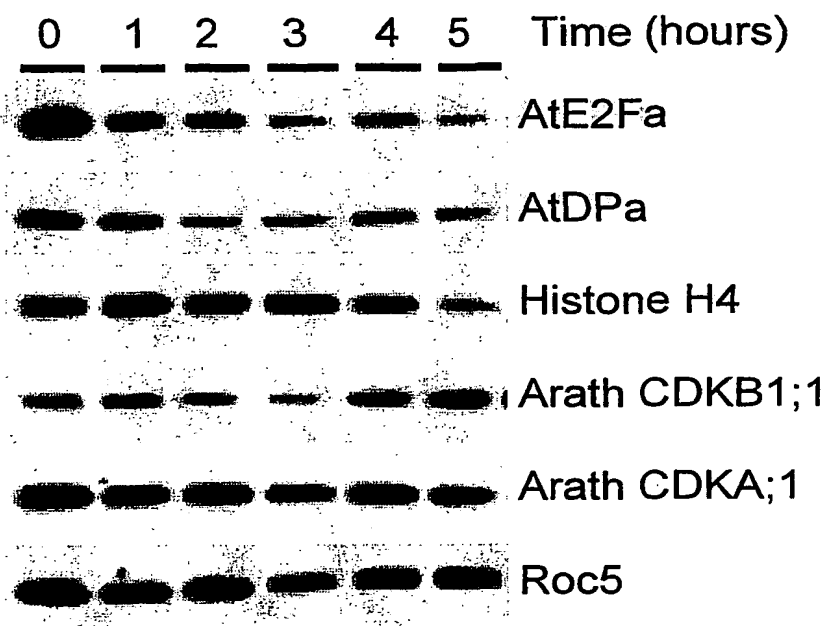


FIGURE 58

63/65

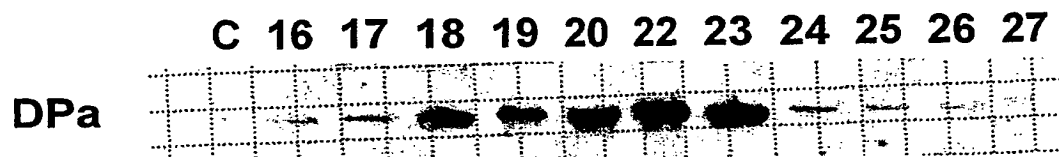


FIGURE 59

64/65

description of molecule	amino acid sequence SEQ ID NO:	nucleic acid sequence SEQ ID NO:
Tag•100 epitope	199	
c-myc epitope	200	
FLAG [®] -epitope	201	
HA epitope	202	
protein C epitope	203	
VSV epitope	204	
DP conserved DNA binding	240	
DP conserved heterodim domain	241	
DP conserved heterodim domain	242	
primer A		243
primer B		244
primer C		245
attB1 site		246
Kozak consensus		247
attB2 site		248
sense E2Fa primer		249
antisense E2Fa primer		250
sense DPa primer		251
antisense DPa primer		252
sense CDKA primer		253
antisense CDKA primer		254
sense CDKB primer		255
antisense CDKB primer		256
sense histone H4 primer		257
antisense histone H4 primer		258
sense roc5 primer		259
antisense roc5 primer		260
sense actin primer		261
antisense actin primer		262
CDK phosphorylation motif CDC2bDN-IC26M	263	

FIGURE 60

65/65

description of molecule	amino acid sequence SEQ ID NO:	nucleic acid sequence SEQ ID NO:
ICK4	264	
forward sequencing primer prm1024		265
reverse sequencing primer prm1025		266
cyclin destruction box	267	
cyclin box consensus motif 1	268	
cyclin box consensus motif 2	269	
CDC2 consensus motif 1	270	
CDC2 consensus motif 2	271	
CDC2 consensus motif 3	272	
CDK phosphorylation site consensus 1	273	
CDK phosphorylation site consensus 2	274	
CDK phosphorylation site consensus 3	275	
CDK phosphorylation site consensus 4	276	
NLS consensus 1	277	
NLS consensus 2	278	
NLS consensus 3	279	
NLS consensus 4	280	
Cy-like box consensus	281	
Rb binding domain consensus 1	282	
Rb binding domain consensus 2	283	
Rb binding domain consensus 3	284	
Rb binding domain consensus 4	285	
DEF domain	286	
DNA binding domain	287	
DCB1 domain consensus 1	288	
DCB1 domain consensus 2	289	
DCB2 domain	290	

FIGURE 60 (continued)

SEQUENCE LISTING

<110> CROPDESIGN N.V.

<120> NUCLEIC ACID MOLECULES ENCODING PLANT CELL CYCLE
PROTEINS AND USES THEREFOR

<130> CNN-001PC

<150> US 60/204,045

<151> 2000-05-12

<160> 290

<170> PatentIn version 3.0

<210> 1

<211> 1255

<212> DNA

<213> Arabidopsis thaliana

<400> 1

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tttgtacaac	atactgaagc	aatgctggag	gagattgaac	agatggagaa	ggagattgaa	180
atggaagatg	cagacaaaga	agaagagcct	gtgatcgata	ttgatgcctg	tgataagaat	240
aatccttttg	ctgcggttga	atatatccat	gatatgcata	ccttctacaa	gaattttgag	300
aaacttagtt	gcgtgcctcc	taactatatg	gacaatcaac	aagatcttaa	tgagagaatg	360
agaggaatcc	tcattgactg	gttaattgag	gtgcactaca	agtttgaact	gatggaggaa	420
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ccatatgttt	tcatgaaacg	atttctcaaa	gctgcccaat	ctgacaagaa	gcttgagatt	720
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tctaagctgg	cggcctcagc	aatctacact	gctcagtgtg	cacttaaggg	atttgaagaa	840
tggaagcaaaa	cctgtgagtt	tcacacaggc	tacaacgaaa	aacagctact	ggcatgtgcg	900
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aagtacaaca	catctaagtt	ctgtcatgct	gcaagaactg	aaccagctgg	gtttctgatt	1020
taatattaat	aagaatctaa	tatgacttaa	ctcgagtttt	tctttagaac	aaaaagagtg	1080
tgagagaaaag	agagatagta	gagcaagttg	cccaaaatgg	gagaagaatg	gatctttaga	1140
tatcatggca	agtagcccaa	aaagagtgtg	ttcttctctt	tctaaggctc	ttagatcttt	1200
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<211> 471

<212> DNA

<213> Arabidopsis thaliana

<400> 2

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gttcttgtcg	ttgatgatga	tccaacttgt	ctcatgatct	tagagaggat	gcttatgact	120
tgtctctaca	gagtaactaa	atgtaacaga	gcagagagcg	cattgtctct	gcttcggaag	180
aacaagaatg	gttttgatat	tgtcattagt	gatgttcata	tgcttgacat	ggatgggttc	240
aagctccttg	aacacgttgg	tttagagatg	gatttacctg	ttatcatgat	gtctgcggat	300
gattcgaaga	gcgttggtgt	gaaaggagtg	actcacggtg	cagttgatta	cctcatcaaa	360

ccggtacgta	ttgaggcttt	gaagaatata	tggcaacatg	tggtgcggaa	gaagcgtaac	420
cgagtggaa	ggttctgaac	attctggagg	aagtattgaa	gatactggcg	g	471

<210> 3
 <211> 1351
 <212> DNA
 <213> Arabidopsis thaliana

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ttggaggata	caagagccac	tggacccaac	aagaggaaga	agcgagcggt	tctaggggag	180
atcacaaatg	ttaactccaa	tacagctata	cttgaggcca	aaaacagcaa	gcagataaag	240
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gtcacagatc	ttcagtcag	gaccgatgca	aaagttgaag	ttgcatcaaa	tacagcagga	360
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cttaaacgca	gaccacttcc	ggactttatg	gagagaatac	agaaggatgt	caccagttcc	660
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caggtcctgg	aaatggagaa	ccaagtactt	aagcatttta	gctttcaa	atacactccc	960
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tcggatctga	aagcatctgt	tcatgcctta	caagatctgc	agcttaacac	caaagggtgc	1260
cccttgagcg	ctatacgc	gaagtatagg	caagagaaat	acaaatctgt	ggcgggttctc	1320
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 <212> DNA
 <213> Arabidopsis thaliana

<400> 4

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cacacgcgtt	gtcttctctg	tagcgcttgt	cagtctctta	cgccgtggaa	agctactggg	180
cttcgtcttg	gcccaacttt	ctccgtctgc	gagtcatg	tcgctcttaa	aaacgccggc	240
ggtggccgtg	gaaacagagt	tttatcggag	aatcgtggtc	aggaggaggt	taatagtttc	300
gagtccgaag	aagatcggat	tagagaagat	cacggtgacg	gtgacgacgc	ggagtcttac	360
gatgatgatg	aggaagaaga	tgaggatgaa	gagtacagcg	acgatgagga	tgaggatgat	420
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caagttcctc	cgggtgatgag	ttcttcatct	tctgacggag	gaagcggagg	ttcagtgacg	540
aagaggacga	gggctagaga	gaattcagat	cttctctgct	ccgatgatga	gatcgggaagc	600
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 <213> Arabidopsis thaliana

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 cgtgtgatta accagaatct cgctggtgca agagtttatc cttgtgttgt caacaagaaa 180
 ggaagcttat tgtctaataa gcaagaagaa gaagaaggat gtcaaaagaa gaagtttgat 240
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 acattggacc ttccaatgcc aatgtcgctt gagaaacat acattgaagc tgatccaatg 420
 gaagaagttg agatggagga tgtaacagtg gaagaaccga tcgtggatat cgatgtctta 480
 gactcgaaga actcgcttgc ggctgttgaa tatgttcaag atctttacgc attttacaga 540
 acaatggaga gatttagttg tgttccagta gactatatga tgcaacaaat cgacttaaac 600
 gagaagatga gagcaatact aatcgactgg ttaatcgagg tacatgacaa gtttgatctg 660
 atgaacgaga cactgtttct gacagtgaat ctgatagata gattcttgtc caagcaaaat 720
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 ttaccgacac aatacccggt cttgaaaaga ttcctcaagg cagctcaagc agacaagaag 960
 tgtgaggtct tggcgtcggt cttgatcgag cttgcccttg tggagtacga gatgcttcgg 1020
 tttccaccat cttactagc tgccacatct gtgtacactg ctcaatgtac acttgatggt 1080
 tccaggaaat ggaacagtac atgtgaattc cattgtcatt actctgaaga ccagctcatg 1140
 gaatgttcac ggaagctggt gagtctgcat cagagggcgg cgacaggaaa cttaacagga 1200
 gtatatagga agtacagcac aagcaaatTT gggtacatag caaaatgtga agctgcacac 1260
 tttctagtgt ctgagtctca tcattct 1287

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 <211> 1078
 <212> DNA
 <213> Arabidopsis thaliana

<400> 6
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 aggacactcg gcgagcggaa acaagcgttt aacgagtatc ttggccaaag gaaaaaagtg 180
 gaagctgagg aaagacgaag gaggcagaag aaagctcggg aagaatttgt caagatgcta 240
 gaggagtgtg aagaactttc atcatccctg aaatggagca aagcaatgag tttgttcgaa 300
 aatgatcagc gttttaaagc tggtgaccgt cctagggatc gtgaagatct ttttgacaat 360
 tacattgtgg aacttgagag gaaggaaaga gaaaaggcag cgagggaaca tcggcagtat 420
 atggcagact atcggaagtt tcttgaaacc tgtgactata tcaaagctgg tacacaatgg 480
 cgcaaaattc aagatagact ggaggatgat gacagatgct catgtcttga aaagatagat 540
 cgtctgattg gttttgagga atacattctt gacctagaga aggaagaaga agagctgaag 600
 agagtagaga aagaacatgt aaggcgggcc gagagaaaaa accgtgatgc atttcgtaca 660
 ctattggaag aacatgttgc tgcaggcatc cttacagcca agacgtactg gttggattat 720
 tgcattgagt taaaagactt gcccacatac caagctgttg catctaatac atctggttca 780
 actccgaaaag acttgtttga agatgtcaca gaagaattag agaagcagta tcatgaggat 840
 aagagctatg tgaaggatgc tatgaagtca agaaagattt ccatggtctc ctctggtgctg 900
 tttgaagatt ttaaatctgc tatttcagaa gatctcagta ctcaacagat atcagacata 960
 aatttaaagc ttatatatga tgacttggtt gggagagtga aggaaaaaga agaaaaagag 1020
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 <211> 511
 <212> DNA

<213> *Arabidopsis thaliana*

<400> 7

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atgcaaggta	agaccgatgg	tgatactatc	attgttatgg	atgcttttgc	tttaccagtg	180
gaaggtagtg	agacaagggt	taatgctcag	gatgatgctt	atgagtacat	ggttgagtat	240
tcacagacca	acaagctcgc	ggggccggct	ggagaatggt	gttggatggg	atcactctca	300
ccctggatat	ggatgctggc	tctccggtat	tgatgtttct	acgcagaggc	ttaaccaaca	360
gcatcaggag	ccatttttag	ctgttggtat	tgatcccaca	aggactgttt	cagctggtaa	420
ggttgagatt	ggtgctttca	gaacatactc	taaaggatat	aaagccctcc	agatgaacct	480
gtttctgagt	atcaaaaacta	ttccttttaa	t			511

<210> 8

<211> 1155

<212> DNA

<213> *Arabidopsis thaliana*

<400> 8

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ctcagcgctc	gctcttctta	agatgggtgg	tcacgctcgc	tctgggtggt	caattgaaat	180
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aaaaaaaaaa	aaaaa					1155

<210> 9

<211> 1308

<212> DNA

<213> *Arabidopsis thaliana*

<400> 9

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gccatggata	ttctggtaga	tatgcataca	gaaaaatcaa	aattagcaga	agatttgtcc	360
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 <212> DNA
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<400> 10						
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aaggcatcac	aatctttgtc	cctaaagatg	atgctttcaa	agctcagaag	aatcctcctt	360
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tctccatggt	tatttccggt	ttggtggcat	tgttcttggt	atcagatggt	tttgagatt	840
gagttatggt	tttaagttac	aatgtgaaa	attgtattac	atcatttgaa	ttgtctttt	900
gatttttgaa	acccattttt	tattatacat	ttttatcatt	attattggtt	gtcattacga	960
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<210> 11
 <211> 643
 <212> DNA
 <213> Arabidopsis thaliana

<400> 11						
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cgtccaggct	gatgtcgaaa	actcacagaa	gaaaaatggt	tacgcaaaga	agatcgattg	180
tgggagtgcg	tgtgtagcac	ggtgcaggct	ttcgaggagg	ccgaggctgt	gtcacagagc	240
gtgcgggact	tgctgctaca	ggtgcaactg	tgtgcctccg	ggtacgtacg	gaaactacga	300
caagtgccag	tgctacgcta	gcctcaccac	ccacggtgga	cgccgcaagt	gcccataaga	360
agaaacaaag	ctcttaattg	ctgcggataa	tgggacgatg	tcgttttggt	agtatttact	420
ttggcgtata	tatgtggatc	gaataataaa	cgagaacgta	cgttgtcggt	gtgagtgtga	480
gtactgtatt	attaatgggt	ctatttgttt	ttacttgcaa	gttttcttgt	tttgaatttg	540
tttttttcat	atttgtatat	cgattcgtgc	attattgtat	tatttcaatt	tgtaataaga	600
ttatgtttacc	tttgagtgggt	tgtttaaaaa	aaaaaaaaaa	aaa		643

<210> 12
 <211> 484
 <212> DNA
 <213> *Arabidopsis thaliana*

<400> 12
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 gtattcaagg aatgcccttt cgagggtggt tacgattatt tgattggtac ctcgagcac 120
 ggcttggtaa ttagttcatc tgagctgaaa ataccaacat ttaggcacct attgattgca 180
 ttggtggac ttgctgggct tgaagaaagt attgaagatg ataatcagta taaggggaaa 240
 aacgttcgag atgtgtttaa tgtatacttg aatacttgtc cacatcaagg tagccgaacc 300
 attcgagcag aggaagcgat gtttatatca cttcagtact tccaggaacc catcagcagg 360
 gcagtgagaa gactttaagc ttcgataaaa agagtcaaag aagctatatt gttctcatag 420
 atctgaggtt tgtctgaaaa agagtgatgt aatgtaactg ttttagaaaa aaaaaaaaaa 480
 aaaa 484

<210> 13
 <211> 688
 <212> DNA
 <213> *Arabidopsis thaliana*

<400> 13
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 taacgaaaat aatcgatgga gactctaaaa agaagaaaaa taagaataag aagaagagaa 120
 gccatgaaga tacggagata gaaccggagc aaaagatgag tctcgacgga gactcgaggg 180
 aggagaagat aaagaagaag aggaagaaca agaaccaaga ggaggagcca gagcttgtga 240
 cggagaaaac gaaagtccaa gaggaggaaa agggaaatgt agaagagggt agagccactg 300
 ttagcatagc catagctggt tcaatcatcc acaacactca atcacttgag ctgcgccacac 360
 gcgtaatctc tctttctctc tatctctccc ttcggtttctc tgtttttcca ttccagata 420
 atttaaagtc cccttcttcc atttctaaca tttctcagct cgccggccaa attgctcgtg 480
 cagctacaat tttccgaatc gacgagatcg tagtggtcga caataagagc agctcagaaa 540
 tcgaatcagc tgctacgaat gcttctgata gcaatgaaa tggtgcctcc tttctcgttc 600
 gtatcttgaa gtatctagag acaccacaat atttgaggaa atctctcttc cccaagcaaa 660
 atgatcttag atatgtgggt atgttgcc 688

<210> 14
 <211> 461
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <221> misc_feature
 <222> 396
 <223> n = a,g,c, or t

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 gcaatgctga gaaatgtttt gggtctcatc aatttcctct acacagtagt gggtctcaat 180
 tactcatccg tcggtttcat gggttttaagc ttgcacgaaa cactagtcgc cttcaagagt 240
 gtatattaca ttggaacagt tatacctatc gctgtgcttc ttctcagcta cttagttcct 300
 gtgaagcctg ttagacaaaa gaccagaaaa gaagaataat gttgtctttt taaaaaatca 360
 acaacatttt gggtcttttc tttttttcca cttggnccgt tttatgtaaa acaagagaaa 420

tcaagatttg aggtttttatt cttaaaaaaa aaaaaaaaaa a

461

<210> 15
 <211> 862
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> 292,294,339
 <223> n = a,g,c, or t

<400> 15
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 caagaacatt ccaacccaaa ctatcaagag cttgatgtat caactatgca aaggtatggc 120
 attctgccat ggtcacggga tattgcacag agatctcaag cctcacaatc tcttgatgga 180
 tccaagaca atgaggctca aaatagcaga tcttggttta gccagagcct tcaactctgcc 240
 aatgaagaag tatacccatg agatattaac tctttggtat agagctccag angnttcttc 300
 ttggtgccac ccattactct acagctgtgg atatgtggnc tgttggtgc atatttgctg 360
 aacttgtgac caaccaagca atctttcagg gagactctga gctccaacag ctctccata 420
 ttttcaagtt gttgggacac ccaatgaaga aatgtgacca ggagtggagca cactcaagaa 480
 ctggcatgaa taccacagt ggaaaccatc gactctatct ctgctgttcc aaacctcgac 540
 gaggtctggag ttgatcttct atctaaaatg ctgcagtacg agccagcgaa acgaatatca 600
 gcaaagatgg ctatggagca tccttacttt gatgatctgc cagaaaagtc ctctctctaa 660
 ggatttaaaa tcttcagtta gtatctttcc aagttttatg gtttttctag ttttgcttct 720
 ttcaagcata tctctagtgt gctgcttccc cctctatgaa tcatccttc tttagcataa 780
 tatatcactt ctgattgttg tttctttcta ttcgaatatt tggattaacg gctttaatgt 840
 tcttaaaaaa aaaaaaaaaa aa 862

<210> 16
 <211> 1114
 <212> DNA
 <213> Arabidopsis thaliana

<400> 16
 acccaaaaga aggatgagta tggagatgga gttgtttgtc actccagaga agcagaggca 60
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 ttctgaaatt ggatcagaga agaaagggca atcaagaact tctggaggcg ggcttcgtca 180
 attcagtgtt atgggtttgtc agaagttgga agccaagaag ataactactt acaaggagggt 240
 tgcagacgaa attattttcag attttgccac aattaagcaa aacgcagaga agcctttgaa 300
 tgaaaatgag tacaatgaga agaacataag gcggagagtc tacgatgcgc tcaatgtggt 360
 catggcgttg gatattattg caagggataa aaaggaaatc cggtggaag gacttcctat 420
 tacctgcaaa aaggatgttg aagaagtcaa gatggatcgt aataaagtta tgagcagtgt 480
 gcaaaagaag gctgcttttc ttaaagagtt gagagaaaag gtctcaagtc ttgagagtct 540
 tatgtcgaga aatcaagaga tggttgtgaa gactcaaggc ccagcagaag gatttacctt 600
 accattcatt ctacttgaga caaacctca cgcagtagtc gaaatcgaga tttctgaaga 660
 tatgcaactt gtacacctcg acttcaatag cacacctttc tcggtccatg atgatgctta 720
 cattttgaaa ctgatgcaag aacagaagca ggaacagaac agagtatctt cttcttcac 780
 tacacatcac caatctcaac atagctccgc tcattcttca tccagttctt gcattgcttc 840
 tggaacctca ggcccggttt gctggaactc gggatccatt gatactcgct gaccgagctt 900
 ctattcccaa attcttcaag aagaagaagt aatgatctaa ttggtatact aaaaaattat 960
 acatctggtt tagtgttcaa ttgagagaga ctgtaaaatc aattcatagg ccaacaaatg 1020
 tttgtttatc caattttcct ttttatcga acttgatgcg atatttcaac ggaaacagaa 1080
 actattgttt taaacaaaaa aaaaaaaaaa aaaa 1114

<210> 17
 <211> 794
 <212> DNA
 <213> Arabidopsis thaliana

<400> 17
 aagatgcaac cgacagagac gtcgcagccg ggcgcgtcgg atcaaggccg ccggcttaag 60
 gatcagttat cggagagtat gagcttcagt agccaaatga agaaggaaga cgatgagttg 120
 tcgatgaaag ctttgtcggc gttcaaggcc aaagaagagg agatcgagaa gaagaagatg 180
 gagatcagag aaagagttca agctcagctt ggtcgtgttg aagatgagtc caagcgtctc 240
 gctatgattc gcgaggaact tgaagggtttt gctgatccca tgaggaagga agttactatg 300
 gtgaggaaga agattgattc tctcgacaaa gaattaaagc cattggggaa tacagttcag 360
 aaaaaggaaa cagagtacaa ggatgctctt gaagcattca atgaaaagaa caaggagaag 420
 gtggagctga tcaccaagct acaggagttg gagggagaaa gcgagaaatt caggttcaag 480
 aagctggagg agctaagcaa gaacattgat ctaaccaaaac cttagtgttg gacgagcaga 540
 gtcgctggga tttggctatt caaagttcta aaaaagtcac ttttagagt attttcattg 600
 ttcttttatg attctagtaa tatatataat ttataaaaata aaaagtaaga agatatgtgt 660
 ttgaactaga tgttgcaaaag aaaatgtaac aaagttacga tggcactaca ttatcgacgt 720
 gattggcaga attgtaatag taatgtaaaag aaactatgtt tgttccggaa aaaaaaaaaa 780
 aaaaaaaaaa aaaa 794

<210> 18
 <211> 448
 <212> DNA
 <213> Arabidopsis thaliana

<400> 18
 cagaaacaag ctccagggtgc aggtgatgtc ccagcaacaa tccaagaaga ggacgatgat 60
 gatgatgtcc cagatcttgt agtgggagag acttttcgaga cccctgctac tgaagaggct 120
 cccaaagctg ctgcttctta gaggaggagg aagaagaagg agaagagctc acctgcaaaa 180
 cccatcataa aaatgtttgt cgctcgacct cttctgagca ctgtcagatt cttgttttct 240
 ctaatgcttg cgaacagaaa gacttggttt tattatcact tgatgctttt tgggtccgaac 300
 agcaattttc cttttattaa ggttagatcg ctttttgttt accacctgtt caaatgagta 360
 ctactatgtc ctgtcgcttc atacacttct tgcaacacag tcctttgttt tgagtcaaaa 420
 aaaaaaaaaa aaaaaaaaaa aaaaaaaa 448

<210> 19
 <211> 1152
 <212> DNA
 <213> Arabidopsis thaliana

<400> 19
 atggaggacg acgacgagat tcagtcaatt ccatctccgg gagattcttc cttttcacca 60
 caagctcctc cttctccgcc gattttgcca acaaacgacg tgacggtggc cgtcgtgaag 120
 aaaccacaac cgggggctttc ttctcaatct ccgtccatga acgcttttagc gttagtgggt 180
 catactcctt ctgtaaccgg tgggtggtgg agcggaaaca gaaacggacg aggaggagga 240
 ggaggaagcg gtggtggtgg aggaggaaga gatgattgtt ggagcgaaga agctacaaag 300
 gttctaactg aagcttgagg agatcgattc tctgaaccag gtaaaggaac tttgaagcaa 360
 caacattgga aagaagtagc tgagattgtg aacaagagtc gtcaatgcaa ataccctaaa 420
 actgatattc agtgtaagaa cagaattgat acggtgaaga agaagtataa gcaagagaaa 480
 gctaagattg cttctggtga tggacctagt aaatgggttt tcttcaagaa gcttgagagt 540
 ttgattggtg gtactacaac attcattgct tcttcaaaaag cttcagagaa ggctcctatg 600
 ggaggagctc ttgggaatag ccgttcgagt atgttttaac ggcaactaa aggtaatcag 660
 attgtgcagc aacaacaaga gaagagaggc tctgattcga tgcggtggca ttttaggaaa 720

cgtagtgctt	ctgagactga	gtctgagtct	gacctgaac	ctgaggcttc	tcctgaggaa	780
tctgctgaga	gtctccacc	tttgcaaccg	attcaaccgc	tttcgtttca	tatgccaaag	840
cgggtgaagg	tggataagag	tggaggtgga	gggagtgag	ttggagatgt	ggcgagggcg	900
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gaactggaaa	aggagaggat	gaaatttgct	aaagagatgg	agttgcagag	aatgcagttc	1020
ttgaaaactc	aattggagat	aacacagaac	aatcaagaag	aggaagagag	gagcaggcag	1080
cgaggagaaa	ggaggatcgt	tgatgatgat	gatgatcgca	atggcaagaa	taacggcaat	1140
gtaagtagct	ga					1152

<210> 20
 <211> 409
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> 201, 344, 365, 369
 <223> n = a, g, c, or t

<400> 20						
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ttcttccatg	gccaccgat	cttcttcttc	ctggccaaac	cccaacccta	atcccgatc	120
cacgtctgcc	tcagattccg	attctacttt	tccctctcac	cgcgatcgcg	tagacgaacc	180
cgactctctc	gattccttct	ntccatgag	tcttaactcc	gacgaacctc	atcagacttc	240
taatcaatcg	cctcttcttc	cccctacgcc	caatttaccg	gtgatgcctc	ctccgttcgt	300
gctttatctt	tcctttaacc	aagatcatgc	ttgcttcgcc	tgtnngcact	gaccgtggct	360
ttacngatnc	ttaattgcga	tcccttctgc	gagattttcc	ggcgggatt		409

<210> 21
 <211> 758
 <212> DNA
 <213> Arabidopsis thaliana

<400> 21						
gtcaggctca	tgattccaga	atagcttgct	tcgctctcac	gcaggatggc	catttggttg	60
ccactgctag	ctctaagggt	actctgggtc	ggatcttcaa	tactgttgat	ggtaccttgc	120
gtcaagaggt	aaggaggggt	gcggatagag	cagagatcta	cagtttggcc	ttctcttcaa	180
atgctcagtg	gttagctgtc	tcaagtgaca	aaggaacggg	ccatgtcttt	ggtctcaaag	240
tcaactccgg	atctcaagtg	aaagactcat	cccgaattgc	acctgatgct	actccctcat	300
ccccatcgtc	gtctctgtct	ttattcaaag	gagtgttacc	gaggtatttc	agctcggagt	360
ggtcggtggc	tcagttcagg	ttggttgaag	gaactcagta	catagccgcc	tttggccatc	420
aaaagaacac	cgttgttatt	cttggcatgg	atgggagctt	ctacagatgc	cagtttgatc	480
cgggtgaacgg	cggtgaaatg	tctcagcttg	agtaccacaa	ctgtctgaaa	ccgccttcag	540
ttttctaaaa	gctttactac	ttatactctt	ttgttctctc	tctctcttta	tatctctctg	600
caacttaagc	ggtgagatat	ggtgtatagt	tttgtgtata	taataatgat	gggtcgtcct	660
ataatttgta	aaacctttta	tcgctaccgc	ggtcgactct	agagccctat	agtgagtcgt	720
attactgcag	agatctatga	atcgtagata	ctgaaaaa			758

<210> 22
 <211> 624
 <212> DNA
 <213> Arabidopsis thaliana

<400> 22

atggactttt	gtgaggtatg	cccggaaaag	cttccaaact	atgaagtgaa	agtgaagagc	60
tttttcgaag	aacattttaca	cactgatgag	gagatccgtt	actgcgttgc	aggaactggt	120
tactttgatg	tgagagatcg	taatgaagct	tggattaggg	tattggtaaa	gaagggaggt	180
atgatagtct	tacctgctgg	gatctatcat	cgcttcactg	tggactctga	caactatatc	240
aaggcaatgc	ggctattcgt	gggtgaaccg	gtatggacac	catacaatcg	cccacacgac	300
catcttcctg	caaggaaaaga	atatgtcgat	aacttcatga	tcaatgcctc	ggcttagaga	360
gcttcctctc	tctatatctg	gctttctgaa	acaaggatct	ataaacaagg	cctacaataa	420
agaaagcttt	cctgtcaagt	attggatatt	tatatgtatt	cctgtgtaga	atgatggctt	480
ttggtagtct	tgagttgttg	taaacttagt	tacactctct	gatatgtctc	tctttaccat	540
ctttgtcgta	tcccatatac	gaaaagatta	cattgggatt	catattgtct	tacgttcgtt	600
cctatgtgca	atatgttgag	tttt				624

<210> 23
 <211> 495
 <212> DNA
 <213> Arabidopsis thaliana

<400> 23	
ccagttttcc	gatcactcgc aagaaaaccc taaaaatgga tggatcatgat tctgaggata 60
ctaagcagag	cactgctgat atgactgctt ttgtccaaaa tcttctccag cagatgcaaa 120
ccaggttcca	gacaatgtcg gactccatca tcacaaagat tgatgacatg ggaggcagaa 180
tcaatgagct	ggagcaaagc atcaatgatc taagagccga gatgggagta gaaggcactc 240
ctcctccagc	ctccaaatca ggcgatgaac ccaaaaacacc ggctagttcc tcttaaaaag 300
gaatgtgggtg	ttcattgaca tgtccgaagg aaaaagaaaa actatgaaat atgttaagag 360
cagtattact	tttaaaattc ctgtttaaga aacgagtttg ttgtttatta aagttcatca 420
aatagattga	tgatgtgggtg cattacatta ttctccacct atgaattgca tttctatattt 480
ggtctaaaaa	aaaaa 495

<210> 24
 <211> 580
 <212> DNA
 <213> Arabidopsis thaliana

<400> 24	
cgcgagagga	cgagcaaaaa tgctcaaaga agttgccacg gagaagcaaaa ccgccgtgga 60
cactcatttc	gcaaccgcta aaaagcttgc tcaagaagga gacgcgttgt tcgttaaaat 120
cttcgcaatc	aagaaactgt tggcgaaaact tgaagcagag aaagaatctg ttgatggaaa 180
gtttaaggag	actgtgaaag aactttctca tcttctggct gatgcttctg aggcttacga 240
agagtatcat	ggcgcggtga ggaaggcgaa agacgagcaa gcggctgagg aatttgcgaa 300
agaggcgacg	caaagtgcag agatcatttg ggttaagttt cttagttctc tttagagaac 360
aattgagatt	cttggttggtg ttaagagcaa atctagagct cttgttggtt cttgttatgt 420
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gggagataga	gagaaagaga gtctctgcga aaactaataa tgttttttca gatatctaaa 540
taataagctt	tttacaaaaa aaaaaaaaaa aaaaaaaaaa 580

<210> 25
 <211> 656
 <212> DNA
 <213> Arabidopsis thaliana

<400> 25	
cgcccgctc	gacgcttgag agattcctct ggctaaaccc agatggagtt tggatctttt 60
cttgtgtcct	tagggacatc ttttgttata ttctgtcattc tcatgcttct cttcacctgg 120
ctttctcgca	aatctggaaa tgctcccatc tattaccgca atcggatcct taaagggctg 180


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gagccatggg aaggcacctc cttgactcga aacccttttg cttggatgcg tgaagctttg 240
acttcctctg aacaagatgt cgtaaactta tccggcgtcg atactgctgt ccactttgtc 300
ttcttgagca ctgttctggg gatatttgct tgttccagtc ttcttctcct accaactcta 360
ctgcctctag ccgctacaga caacaacata aagaacacaa agaatgcgac agataccaca 420
agcaaaggaa ctttttagcca acttgataat ctatcaatgg ctaacatcac aaaaaaaagt 480
tcgaggctgt gggcgttcct aggagctggt tactggatat ctttggtcac atatttcttc 540
ttgtggaaag cttataagca tgtctcttca ttgagagctc aagctctgat gtctgctgat 600
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<210> 26
<211> 985
<212> DNA
<213> Arabidopsis thaliana

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<400> 26
gttcacactc cggctgggtga actgcaaaga cagattaggt catggcttgc agaaagtttt 60
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ctttccacag caattatgga tggctggatg gctggagtag gagctccggt gcctcctcac 180
acagacgctt taggacagct tgtgtctgag tatgcaaagc gagtctacac ttctcagatg 240
cagcatctaa aggatattgc cggtaactttg gcttcggaag aggcagaaga tgctgggtcaa 300
gtcgcgaagc ttcgatcagc tctcgagtct gttgaccaca aaagaagaaa gattttgcaa 360
caaatagagaa gtgatgcagc tttgtttacc ttggaagaag gcagttcccc tgttcaaaat 420
ccatctacag cagccgaaga ctcgagatta gcctccctca tttctctgga tgccatactg 480
aagcaagtca aggaaataac aagacaagcc tctgtccacg ttttgagtaa aagcaagaaa 540
aaggcattgc ttgagtctct tgatgaactt aacgaacgaa tgccttctct gcttgatggt 600
gatcatccat gtgcacagag agaaattgat acggctcacc agttggtcga gacaattcca 660
gaacaagagg acaatcttca agacgaaaag agaccttcaa tagattcaat atcttcgact 720
gaaaccgatg tgtctcaatg gaatgttttg caattcaaca caggaggctc tttagctcca 780
ttcatcataa aatgcggagc taactccaac tcagagctcg tgatcaaagc ggatgcccg 840
attcaagaac ctaaaggagg cgaaatagtg agagttgtgc caagaccttc ggtttttagaa 900
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ctggccttag ctagaacagc tgatg 985

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<210> 27
<211> 527
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> misc_feature
<222> 512
<223> n = a,g,c, or t

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<400> 27
acttatgaga ggttaccgat tgaggaagaa caacagcaag agcagccgct tcaactagaa 60
gatgggaaga agcagaaaga agagaatgat gataacgaga gtgggaataa cggaaacgaa 120
ggatcgatgc agccgccgat gtataatatg cctcctaatt ttatcccaa tggatcatcaa 180
atggctcaac acgacgtgta ttgggggtgg cctccgcctc gtgctcctcc ttcgatttga 240
ttaagttaga taggcggtgg ttggtgcgtt ctttttactg gaatgattat attttccatt 300
aggatgggta ggcttttgtt attaaagcta tcaagtttct ttttttttac ggataattcg 360
gatgacaatt agctagtgtt tgtttgtttg ttttgtggcc ggcttttctg cttgactatt 420
ttgatcgcg atagctttgt atgaaagtga attgattgta gaatcgtctt ttgaattttg 480
atgttgga aaaccaagca atggtgtgtg gnccttgc aa tggaagc 527

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<210> 28
 <211> 610
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <221> misc_feature
 <222> 482, 494, 495, 516, 560, 567, 587, 607
 <223> n = a, g, c, or t

<400> 28
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 acagattgaa gaactgaaag gattgaacct tgttgagaaa gatggtggtt catcttcttc 120
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 <212> DNA
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<211> 2289

<212> DNA

<213> Arabidopsis thaliana

<400> 36

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<211> 1094

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<213> Arabidopsis thaliana

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 <212> DNA
 <213> Arabidopsis thaliana

<400> 42

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<211> 1260

<212> DNA

<213> Arabidopsis thaliana

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 <213> Arabidopsis thaliana

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 <212> DNA
 <213> Arabidopsis thaliana

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 <223> n = a,g,c, or t

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<212> DNA
<213> Arabidopsis thaliana

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<220>
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<223> n = a,g,c, or t

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 <211> 1142
 <212> DNA
 <213> Arabidopsis thaliana

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 <212> DNA
 <213> Arabidopsis thaliana

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<211> 865

<212> DNA

<213> Arabidopsis thaliana

<400> 58

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<210> 59

<211> 723

<212> DNA

<213> *Arabidopsis thaliana*

<220>

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<222> 559,622,677

<223> n = a,g,c, or t

<400> 59

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<210> 60

<211> 426

<212> DNA

<213> *Arabidopsis thaliana*

<400> 60

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<210> 61

<211> 1442

<212> DNA

<213> *Arabidopsis thaliana*

<400> 61

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<210> 62

<211> 1506

<212> DNA

<213> Arabidopsis thaliana

<400> 62

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<210> 63

<211> 2631

<212> DNA

<213> Arabidopsis thaliana

<400> 63

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Pro	Arg	Pro	Leu	Gly	Arg	Ser	Ala	Ser	Thr	Ala	Glu	Lys	Ser	Ala	Val	
145				150						155					160	
Ile	Gly	Ser	Ser	Thr	Val	Pro	Asp	Ile	Pro	Lys	Phe	Val	Asp	Ile	Asp	
				165				170						175		
Ser	Asp	Asp	Lys	Asp	Pro	Leu	Leu	Cys	Cys	Leu	Tyr	Ala	Pro	Glu	Ile	
			180					185					190			
His	Tyr	Asn	Leu	Arg	Val	Ser	Glu	Leu	Lys	Arg	Arg	Pro	Leu	Pro	Asp	
		195					200					205				
Phe	Met	Glu	Arg	Ile	Gln	Lys	Asp	Val	Thr	Gln	Ser	Met	Arg	Gly	Ile	
	210				215						220					
Leu	Val	Asp	Trp	Leu	Val	Glu	Val	Ser	Glu	Glu	Tyr	Thr	Leu	Ala	Ser	
225				230						235					240	
Asp	Thr	Leu	Tyr	Leu	Thr	Val	Tyr	Leu	Ile	Asp	Trp	Phe	Leu	His	Gly	
				245				250						255		
Asn	Tyr	Val	Gln	Arg	Gln	Gln	Leu	Gln	Leu	Leu	Gly	Ile	Thr	Cys	Met	
			260					265					270			
Leu	Ile	Ala	Ser	Lys	Tyr	Glu	Glu	Ile	Ser	Ala	Pro	Arg	Ile	Glu	Glu	
		275					280					285				
Phe	Cys	Phe	Ile	Thr	Asp	Asn	Thr	Tyr	Thr	Arg	Asp	Gln	Val	Leu	Glu	
	290					295					300					
Met	Glu	Asn	Gln	Val	Leu	Lys	His	Phe	Ser	Phe	Gln	Ile	Tyr	Thr	Pro	
305					310					315					320	
Thr	Pro	Lys	Thr	Phe	Leu	Arg	Arg	Phe	Leu	Arg	Ala	Ala	Gln	Ala	Ser	
				325				330						335		
Arg	Leu	Ser	Pro	Ser	Leu	Glu	Val	Glu	Phe	Leu	Ala	Ser	Tyr	Leu	Thr	
			340					345					350			
Glu	Leu	Thr	Leu	Ile	Asp	Tyr	His	Phe	Leu	Lys	Phe	Leu	Pro	Ser	Val	
		355					360					365				
Val	Ala	Ala	Ser	Ala	Gly	Phe	Leu	Ala	Lys	Trp	Thr	Met	Asp	Gln	Ser	
	370				375						380					
Asn	His	Pro	Trp	Asn	Pro	Thr	Leu	Glu	His	Tyr	Thr	Thr	Tyr	Lys	Ala	
385				390						395					400	
Ser	Asp	Leu	Lys	Ala	Ser	Val	His	Ala	Leu	Gln	Asp	Leu	Gln	Leu	Asn	
			405					410						415		
Thr	Lys	Gly	Cys	Pro	Leu	Ser	Ala	Ile	Arg	Met	Lys	Tyr	Arg	Gln	Glu	
		420					425						430			
Lys	Tyr	Lys	Ser	Val	Ala	Val	Leu	Thr	Ser	Pro	Lys	Leu	Leu	Asp	Thr	
		435			</											

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<210> 70
<211> 223
<212> PRT
<213> Arabidopsis thaliana
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<400>      70
Met Gly Lys Lys Cys Asp Leu Cys Asn Gly Val Ala Arg Met Tyr Cys
1          5          10          15
Glu Ser Asp Gln Ala Ser Leu Cys Trp Asp Cys Asp Gly Lys Val His
          20          25          30

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Gly Ala Asn Phe Leu Val Ala Lys His Thr Arg Cys Leu Leu Cys Ser
 35 40 45
 Ala Cys Gln Ser Leu Thr Pro Trp Lys Ala Thr Gly Leu Arg Leu Gly
 50 55 60
 Pro Thr Phe Ser Val Cys Glu Ser Cys Val Ala Leu Lys Asn Ala Gly
 65 70 75 80
 Gly Gly Arg Gly Asn Arg Val Leu Ser Glu Asn Arg Gly Gln Glu Glu
 85 90 95
 Val Asn Ser Phe Glu Ser Glu Glu Asp Arg Ile Arg Glu Asp His Gly
 100 105 110
 Asp Gly Asp Asp Ala Glu Ser Tyr Asp Asp Asp Glu Glu Asp Glu
 115 120 125
 Asp Glu Glu Tyr Ser Asp Asp Glu Asp Glu Asp Asp Asp Glu Asp Gly
 130 135 140
 Asp Asp Glu Glu Ala Glu Asn Gln Val Val Pro Trp Ser Ala Ala Ala
 145 150 155 160
 Gln Val Pro Pro Val Met Ser Ser Ser Ser Ser Asp Gly Gly Ser Gly
 165 170 175
 Gly Ser Val Thr Lys Arg Thr Arg Ala Arg Glu Asn Ser Asp Leu Leu
 180 185 190
 Cys Ser Asp Asp Glu Ile Gly Ser Ser Ser Ala Gln Gly Ser Asn Tyr
 195 200 205
 Ser Arg Pro Leu Lys Arg Ser Ala Phe Lys Ser Thr Val Val Val
 210 215 220

<210> 71
 <211> 429
 <212> PRT
 <213> Arabidopsis thaliana

<400> 71
 Met Val Asn Ser Cys Glu Asn Lys Ile Phe Val Lys Pro Thr Ser Thr
 1 5 10 15
 Thr Ile Leu Gln Asp Glu Thr Arg Ser Arg Lys Phe Gly Gln Glu Met
 20 25 30
 Lys Arg Glu Lys Arg Arg Val Leu Arg Val Ile Asn Gln Asn Leu Ala
 35 40 45
 Gly Ala Arg Val Tyr Pro Cys Val Val Asn Lys Lys Gly Ser Leu Leu
 50 55 60
 Ser Asn Lys Gln Glu Glu Glu Glu Gly Cys Gln Lys Lys Lys Phe Asp
 65 70 75 80
 Ser Leu Arg Pro Ser Val Thr Arg Ser Gly Val Glu Glu Glu Thr Asn
 85 90 95
 Lys Lys Leu Lys Pro Ser Val Pro Ser Ala Asn Asp Phe Gly Asp Cys
 100 105 110
 Ile Phe Ile Asp Glu Glu Glu Ala Thr Leu Asp Leu Pro Met Pro Met
 115 120 125
 Ser Leu Glu Lys Pro Tyr Ile Glu Ala Asp Pro Met Glu Glu Val Glu
 130 135 140
 Met Glu Asp Val Thr Val Glu Glu Pro Ile Val Asp Ile Asp Val Leu
 145 150 155 160
 Asp Ser Lys Asn Ser Leu Ala Ala Val Glu Tyr Val Gln Asp Leu Tyr
 165 170 175
 Ala Phe Tyr Arg Thr Met Glu Arg Phe Ser Cys Val Pro Val Asp Tyr
 180 185 190
 Met Met Gln Gln Ile Asp Leu Asn Glu Lys Met Arg Ala Ile Leu Ile

	195		200		205										
Asp	Trp	Leu	Ile	Glu	Val	His	Asp	Lys	Phe	Asp	Leu	Met	Asn	Glu	Thr
	210					215					220				
Leu	Phe	Leu	Thr	Val	Asn	Leu	Ile	Asp	Arg	Phe	Leu	Ser	Lys	Gln	Asn
225					230					235					240
Val	Met	Arg	Lys	Lys	Leu	Gln	Leu	Val	Gly	Leu	Val	Ala	Leu	Leu	Leu
				245					250					255	
Ala	Cys	Lys	Tyr	Glu	Glu	Val	Ser	Val	Pro	Val	Val	Glu	Asp	Leu	Val
			260					265					270		
Leu	Ile	Ser	Asp	Lys	Ala	Tyr	Thr	Arg	Asn	Asp	Val	Leu	Glu	Met	Glu
		275					280					285			
Lys	Thr	Met	Leu	Ser	Thr	Leu	Gln	Phe	Asn	Ile	Ser	Leu	Pro	Thr	Gln
	290					295					300				
Tyr	Pro	Phe	Leu	Lys	Arg	Phe	Leu	Lys	Ala	Ala	Gln	Ala	Asp	Lys	Lys
305					310					315					320
Cys	Glu	Val	Leu	Ala	Ser	Phe	Leu	Ile	Glu	Leu	Ala	Leu	Val	Glu	Tyr
				325					330					335	
Glu	Met	Leu	Arg	Phe	Pro	Pro	Ser	Leu	Leu	Ala	Ala	Thr	Ser	Val	Tyr
			340					345					350		
Thr	Ala	Gln	Cys	Thr	Leu	Asp	Gly	Ser	Arg	Lys	Trp	Asn	Ser	Thr	Cys
		355					360					365			
Glu	Phe	His	Cys	His	Tyr	Ser	Glu	Asp	Gln	Leu	Met	Glu	Cys	Ser	Arg
	370					375					380				
Lys	Leu	Val	Ser	Leu	His	Gln	Arg	Ala	Ala	Thr	Gly	Asn	Leu	Thr	Gly
385					390					395					400
Val	Tyr	Arg	Lys	Tyr	Ser	Thr	Ser	Lys	Phe	Gly	Tyr	Ile	Ala	Lys	Cys
				405					410					415	
Glu	Ala	Ala	His	Phe	Leu	Val	Ser	Glu	Ser	His	His	Ser			
			420					425							

<210> 72

<211> 359

<212> PRT

<213> Arabidopsis thaliana

<400> 72

Thr	Lys	Gln	Glu	Ala	Lys	Ala	Ala	Phe	Lys	Ser	Leu	Leu	Glu	Ser	Val
1				5				10					15		
Asn	Val	His	Ser	Asp	Trp	Thr	Trp	Glu	Gln	Thr	Leu	Lys	Glu	Ile	Val
			20					25					30		
His	Asp	Lys	Arg	Tyr	Gly	Ala	Leu	Arg	Thr	Leu	Gly	Glu	Arg	Lys	Gln
		35				40					45				
Ala	Phe	Asn	Glu	Tyr	Leu	Gly	Gln	Arg	Lys	Lys	Val	Glu	Ala	Glu	Glu
	50					55					60				
Arg	Arg	Arg	Arg	Gln	Lys	Lys	Ala	Arg	Glu	Glu	Phe	Val	Lys	Met	Leu
65					70				75						80
Glu	Glu	Cys	Glu	Glu	Leu	Ser	Ser	Ser	Leu	Lys	Trp	Ser	Lys	Ala	Met
				85				90						95	
Ser	Leu	Phe	Glu	Asn	Asp	Gln	Arg	Phe	Lys	Ala	Val	Asp	Arg	Pro	Arg
			100					105					110		
Asp	Arg	Glu	Asp	Leu	Phe	Asp	Asn	Tyr	Ile	Val	Glu	Leu	Glu	Arg	Lys
		115					120					125			
Glu	Arg	Glu	Lys	Ala	Ala	Glu	Glu	His	Arg	Gln	Tyr	Met	Ala	Asp	Tyr
	130					135					140				
Arg	Lys	Phe	Leu	Glu	Thr	Cys	Asp	Tyr	Ile	Lys	Ala	Gly	Thr	Gln	Trp
145					150					155					160

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Arg Lys Ile Gln Asp Arg Leu Glu Asp Asp Asp Arg Cys Ser Cys Leu
      165                      170                      175
Glu Lys Ile Asp Arg Leu Ile Gly Phe Glu Glu Tyr Ile Leu Asp Leu
      180                      185                      190
Glu Lys Glu Glu Glu Glu Leu Lys Arg Val Glu Lys Glu His Val Arg
      195                      200                      205
Arg Ala Glu Arg Lys Asn Arg Asp Ala Phe Arg Thr Leu Leu Glu Glu
      210                      215                      220
His Val Ala Ala Gly Ile Leu Thr Ala Lys Thr Tyr Trp Leu Asp Tyr
      225                      230                      235                      240
Cys Ile Glu Leu Lys Asp Leu Pro Gln Tyr Gln Ala Val Ala Ser Asn
      245                      250                      255
Thr Ser Gly Ser Thr Pro Lys Asp Leu Phe Glu Asp Val Thr Glu Glu
      260                      265                      270
Leu Glu Lys Gln Tyr His Glu Asp Lys Ser Tyr Val Lys Asp Ala Met
      275                      280                      285
Lys Ser Arg Lys Ile Ser Met Val Ser Ser Trp Leu Phe Glu Asp Phe
      290                      295                      300
Lys Ser Ala Ile Ser Glu Asp Leu Ser Thr Gln Gln Ile Ser Asp Ile
      305                      310                      315                      320
Asn Leu Lys Leu Ile Tyr Asp Asp Leu Val Gly Arg Val Lys Glu Lys
      325                      330                      335
Glu Glu Lys Glu Ala Arg Lys Leu Gln Arg Leu Ala Glu Glu Phe Thr
      340                      345                      350
Asn Leu Leu His Thr Phe Lys
      355

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<210> 73
<211> 110
<212> PRT
<213> Arabidopsis thaliana

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<400> 73
Gln Glu Lys Pro Trp Glu Asn Asp Pro His Tyr Phe Lys Arg Val Lys
1      5      10
Ile Ser Ala Leu Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly
      20      25      30
Gly Thr Ile Glu Ile Met Gly Leu Met Gln Gly Lys Thr Asp Gly Asp
      35      40      45
Thr Ile Ile Val Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu
      50      55      60
Thr Arg Val Asn Ala Gln Asp Asp Ala Tyr Glu Tyr Met Val Glu Tyr
      65      70      75      80
Ser Gln Thr Asn Lys Leu Ala Gly Pro Ala Gly Glu Cys Cys Trp Met
      85      90      95
Val Ser Leu Ser Pro Trp Ile Trp Met Leu Ala Leu Arg Tyr
      100      105      110

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<210> 74
<211> 337
<212> PRT
<213> Arabidopsis thaliana

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<400> 74
Val Asp Ser Pro Asp Ser Thr Ser Asp Asn Ile Phe Tyr Tyr Asp Asp

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1 5 10 15
 Thr Ser Gln Thr Arg Phe Gln Gln Glu Lys Pro Trp Glu Asn Asp Pro
 20 25 30
 His Tyr Phe Lys Arg Val Lys Ile Ser Ala Leu Ala Leu Leu Lys Met
 35 40 45
 Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu Met
 50 55 60
 Gln Gly Lys Thr Asp Gly Asp Thr Ile Ile Val Met Asp Ala Phe Ala
 65 70 75 80
 Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Asp Asp Ala
 85 90 95
 Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Asn Lys Leu Ala Gly Arg
 100 105 110
 Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly Cys
 115 120 125
 Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Arg Leu Asn Gln Gln His
 130 135 140
 Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val Ser
 145 150 155 160
 Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Ser Lys Gly Tyr
 165 170 175
 Lys Pro Pro Asp Glu Pro Val Ser Glu Tyr Gln Thr Ile Pro Leu Asn
 180 185 190
 Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu Asp
 195 200 205
 Val Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu Leu
 210 215 220
 Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu Gly
 225 230 235 240
 Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys Leu
 245 250 255
 Glu Gln Ala Glu Ser His Leu Val Gln Ser Arg Phe Gly Gly Val Val
 260 265 270
 Pro Ser Ser Leu His Lys Lys Lys Glu Asp Glu Ser Gln Leu Thr Lys
 275 280 285
 Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln Val His Gly Leu
 290 295 300
 Met Ser Gln Val Ile Lys Asp Glu Leu Phe Asn Ser Met Arg Gln Ser
 305 310 315 320
 Asn Asn Lys Ser Pro Thr Asp Ser Ser Asp Pro Asp Pro Met Ile Thr
 325 330 335
 Tyr

<210> 75

<211> 436

<212> PRT

<213> Arabidopsis thaliana

<400> 75

Met Tyr Cys Ser Ser Ser Met His Pro Asn Ala Asn Lys Glu Asn Ile
 1 5 10 15
 Ser Thr Ser Asp Val Gln Glu Ser Phe Val Arg Ile Thr Arg Ser Arg
 20 25 30
 Ala Lys Lys Ala Met Gly Arg Gly Val Ser Ile Pro Pro Thr Lys Pro
 35 40 45

Ser	Phe	Lys	Gln	Gln	Lys	Arg	Arg	Ala	Val	Leu	Lys	Asp	Val	Ser	Asn
50						55					60				
Thr	Ser	Ala	Asp	Ile	Ile	Tyr	Ser	Glu	Leu	Arg	Lys	Gly	Gly	Asn	Ile
65						70					75				80
Lys	Ala	Asn	Arg	Lys	Cys	Leu	Lys	Glu	Pro	Lys	Lys	Ala	Ala	Lys	Glu
						85									95
Gly	Ala	Asn	Ser	Ala	Met	Asp	Ile	Leu	Val	Asp	Met	His	Thr	Glu	Lys
															110
Ser	Lys	Leu	Ala	Glu	Asp	Leu	Ser	Lys	Ile	Arg	Met	Ala	Glu	Ala	Gln
															125
Asp	Val	Ser	Leu	Ser	Asn	Phe	Lys	Asp	Glu	Glu	Ile	Thr	Glu	Gln	Gln
															140
Glu	Asp	Gly	Ser	Gly	Val	Met	Glu	Leu	Leu	Gln	Val	Val	Asp	Ile	Asp
145						150									160
Ser	Asn	Val	Glu	Asp	Pro	Gln	Cys	Cys	Ser	Leu	Tyr	Ala	Ala	Asp	Ile
															175
Tyr	Asp	Asn	Ile	His	Val	Ala	Glu	Leu	Gln	Gln	Arg	Pro	Leu	Ala	Asn
															190
Tyr	Met	Glu	Leu	Val	Gln	Arg	Asp	Ile	Asp	Pro	Asp	Met	Arg	Lys	Ile
															205
Leu	Ile	Asp	Trp	Leu	Val	Glu	Val	Ser	Asp	Asp	Tyr	Lys	Leu	Val	Pro
															220
Asp	Thr	Leu	Tyr	Leu	Thr	Val	Asn	Leu	Ile	Asp	Arg	Phe	Leu	Ser	Asn
225						230									240
Ser	Tyr	Ile	Glu	Arg	Gln	Arg	Leu	Gln	Leu	Leu	Gly	Val	Ser	Cys	Met
															255
Leu	Ile	Ala	Ser	Lys	Tyr	Glu	Glu	Leu	Ser	Ala	Pro	Gly	Val	Glu	Glu
															270
Phe	Cys	Phe	Ile	Thr	Ala	Asn	Thr	Tyr	Thr	Arg	Arg	Glu	Val	Leu	Ser
															285
Met	Glu	Ile	Gln	Ile	Leu	Asn	Phe	Val	His	Phe	Arg	Leu	Ser	Val	Pro
															300
Thr	Thr	Lys	Thr	Phe	Leu	Arg	Arg	Phe	Ile	Lys	Ala	Ala	Gln	Ala	Ser
305						310									320
Tyr	Lys	Val	Pro	Phe	Ile	Glu	Leu	Glu	Tyr	Leu	Ala	Asn	Tyr	Leu	Ala
															335
Glu	Leu	Thr	Leu	Val	Glu	Tyr	Ser	Phe	Leu	Arg	Phe	Leu	Pro	Ser	Leu
															350
Ile	Ala	Ala	Ser	Ala	Val	Phe	Leu	Ala	Arg	Trp	Thr	Leu	Asp	Gln	Thr
															365
Asp	His	Pro	Trp	Asn	Pro	Thr	Leu	Gln	His	Tyr	Thr	Arg	Tyr	Glu	Val
															380
Ala	Glu	Leu	Lys	Asn	Thr	Val	Leu	Ala	Met	Glu	Asp	Leu	Gln	Leu	Asn
385						390									400
Thr	Ser	Gly	Cys	Thr	Leu	Ala	Ala	Thr	Arg	Glu	Lys	Tyr	Asn	Gln	Pro
															415
Lys	Phe	Lys	Ser	Val	Ala	Lys	Leu	Thr	Ser	Pro	Lys	Arg	Val	Thr	Leu
															430
Leu	Phe	Ser	Arg												
															435

<210> 76

<211> 254

<212> PRT

<213> Arabidopsis thaliana

<400> 76

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Met Ala Lys Met Gln Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile
1      5      10      15
Val Cys Ser Ala Ser Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu
20      25      30
Pro Pro Thr Pro Ala Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr
35      40      45
Glu Leu Leu Ser Val Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu
50      55      60
Leu Ser Thr Gly Val Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr
65      70      75      80
Glu Glu Gly Ile Thr Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala
85      90      95
Gln Lys Asn Pro Pro Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln
100     105     110
Leu Val Leu Phe His Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe
115     120     125
Lys Asn Leu Ser Gln Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln
130     135     140
Tyr Ser Leu Lys Phe Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser
145     150     155     160
Leu Trp Thr Arg Thr Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro
165     170     175
Val Ala Val Tyr Gln Val Asn Arg Val Leu Leu Pro Glu Ala Ile Phe
180     185     190
Gly Thr Asp Val Pro Pro Met Pro Ala Pro Ala Pro Ile Val
195     200     205
Ser Ala Pro Ser Asp Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser
210     215     220
Ser Pro Lys Ser Ser His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala
225     230     235     240
Pro Ile Ser Met Val Ile Ser Gly Leu Val Ala Leu Phe Leu
245     250

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<210> 77

<211> 86

<212> PRT

<213> Arabidopsis thaliana

<400> 77

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Met Ala Ile Ser Lys Ala Leu Ile Ala Ser Phe Leu Ile Ser Leu Leu
1      5      10      15
Val Leu Gln Leu Val Gln Ala Asp Val Glu Asn Ser Gln Lys Asn
20      25      30
Gly Tyr Ala Lys Lys Ile Asp Cys Gly Ser Ala Cys Val Ala Arg Leu
35      40      45
Gln Ala Phe Glu Glu Ala Glu Ala Val Ser Gln Ser Val Arg Asp Leu
50      55      60
Leu Leu Gln Val Gln Leu Cys Ala Ser Gly Tyr Val Arg Lys Leu Arg
65      70      75      80
Gln Val Pro Val Leu Arg
85

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<210> 78

<211> 125

<212> PRT

<213> Arabidopsis thaliana

<400> 78

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Lys Glu Glu Ala Gly Met Tyr Trp Gly Tyr Lys Val Arg Tyr Ala Ser
1      5      10      15
Gln Leu Ser Ser Val Phe Lys Glu Cys Pro Phe Glu Gly Gly Tyr Asp
      20      25      30
Tyr Leu Ile Gly Thr Ser Glu His Gly Leu Val Ile Ser Ser Glu
      35      40      45
Leu Lys Ile Pro Thr Phe Arg His Leu Leu Ile Ala Phe Gly Gly Leu
      50      55      60
Ala Gly Leu Glu Glu Ser Ile Glu Asp Asp Asn Gln Tyr Lys Gly Lys
65      70      75      80
Asn Val Arg Asp Val Phe Asn Val Tyr Leu Asn Thr Cys Pro His Gln
      85      90      95
Gly Ser Arg Thr Ile Arg Ala Glu Glu Ala Met Phe Ile Ser Leu Gln
      100      105      110
Tyr Phe Gln Glu Pro Ile Ser Arg Ala Val Arg Arg Leu
      115      120      125

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<210> 79

<211> 231

<212> PRT

<213> Arabidopsis thaliana

<400> 79

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Ala Arg Glu Met Gly Lys Lys Asn Lys Arg Ser Gln Asp Glu Ser Glu
1      5      10      15
Leu Glu Leu Glu Pro Glu Leu Thr Lys Ile Ile Asp Gly Asp Ser Lys
      20      25      30
Lys Lys Lys Asn Lys Asn Lys Lys Lys Arg Ser His Glu Asp Thr Glu
      35      40      45
Ile Glu Pro Glu Gln Lys Met Ser Leu Asp Gly Asp Ser Arg Glu Glu
      50      55      60
Lys Ile Lys Lys Lys Arg Lys Asn Lys Asn Gln Glu Glu Glu Pro Glu
65      70      75      80
Leu Val Thr Glu Lys Thr Lys Val Gln Glu Glu Lys Gly Asn Val
      85      90      95
Glu Glu Gly Arg Ala Thr Val Ser Ile Ala Ile Ala Gly Ser Ile Ile
      100      105      110
His Asn Thr Gln Ser Leu Glu Leu Ala Thr Arg Val Ile Ser Leu Ser
      115      120      125
Leu Tyr Leu Ser Leu Arg Phe Ser Val Phe Pro Phe Pro Asp Asn Leu
      130      135      140
Lys Ser Pro Ser Ser Ile Ser Asn Ile Ser Gln Leu Ala Gly Gln Ile
145      150      155      160
Ala Arg Ala Ala Thr Ile Phe Arg Ile Asp Glu Ile Val Val Phe Asp
      165      170      175
Asn Lys Ser Ser Ser Glu Ile Glu Ser Ala Ala Thr Asn Ala Ser Asp
      180      185      190
Ser Asn Glu Ser Gly Ala Ser Phe Leu Val Arg Ile Leu Lys Tyr Leu
      195      200      205
Glu Thr Pro Gln Tyr Leu Arg Lys Ser Leu Phe Pro Lys Gln Asn Asp
      210      215      220
Leu Arg Tyr Val Gly Met Leu

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225

230

<210> 80
 <211> 112
 <212> PRT
 <213> Arabidopsis thaliana

<400> 80
 Val Ser Ala Val Trp His Gly Leu Tyr Pro Gly Tyr Ile Ile Phe Phe
 1 5 10 15
 Val Gln Ser Ala Leu Met Ile Asp Gly Ser Lys Ala Ile Tyr Arg Trp
 20 25 30
 Gln Gln Ala Ile Pro Pro Lys Met Ala Met Leu Arg Asn Val Leu Val
 35 40 45
 Leu Ile Asn Phe Leu Tyr Thr Val Val Val Leu Asn Tyr Ser Ser Val
 50 55 60
 Gly Phe Met Val Leu Ser Leu His Glu Thr Leu Val Ala Phe Lys Ser
 65 70 75 80
 Val Tyr Tyr Ile Gly Thr Val Ile Pro Ile Ala Val Leu Leu Leu Ser
 85 90 95
 Tyr Leu Val Pro Val Lys Pro Val Arg Pro Lys Thr Arg Lys Glu Glu
 100 105 110

<210> 81
 <211> 119
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> VARIANT
 <222> 97,98,113
 <223> Xaa = any amino acid

<400> 81
 Val Phe Glu Tyr Met Asp Thr Asp Val Lys Lys Phe Ile Arg Ser Phe
 1 5 10 15
 Arg Ser Thr Gly Lys Asn Ile Pro Thr Gln Thr Ile Lys Ser Leu Met
 20 25 30
 Tyr Gln Leu Cys Lys Gly Met Ala Phe Cys His Gly His Gly Ile Leu
 35 40 45
 His Arg Asp Leu Lys Pro His Asn Leu Leu Met Asp Pro Lys Thr Met
 50 55 60
 Arg Leu Lys Ile Ala Asp Leu Gly Leu Ala Arg Ala Phe Thr Leu Pro
 65 70 75 80
 Met Lys Lys Tyr Thr His Glu Ile Leu Thr Leu Trp Tyr Arg Ala Pro
 85 90 95
 Xaa Xaa Ser Ser Trp Cys His Pro Leu Leu Tyr Ser Cys Gly Tyr Val
 100 105 110
 Xaa Cys Trp Leu His Ile Cys
 115

<210> 82
 <211> 296
 <212> PRT

<213> Arabidopsis thaliana

<400> 82

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Pro Lys Arg Arg Met Ser Met Glu Met Glu Leu Phe Val Thr Pro Glu
1      5      10      15
Lys Gln Arg Gln His Pro Ser Val Ser Val Glu Lys Thr Pro Val Arg
      20      25      30
Arg Lys Leu Ile Val Asp Asp Asp Ser Glu Ile Gly Ser Glu Lys Lys
      35      40      45
Gly Gln Ser Arg Thr Ser Gly Gly Gly Leu Arg Gln Phe Ser Val Met
      50      55      60
Val Cys Gln Lys Leu Glu Ala Lys Lys Ile Thr Thr Tyr Lys Glu Val
      65      70      75      80
Ala Asp Glu Ile Ile Ser Asp Phe Ala Thr Ile Lys Gln Asn Ala Glu
      85      90      95
Lys Pro Leu Asn Glu Asn Glu Tyr Asn Glu Lys Asn Ile Arg Arg Arg
      100      105      110
Val Tyr Asp Ala Leu Asn Val Phe Met Ala Leu Asp Ile Ile Ala Arg
      115      120      125
Asp Lys Lys Glu Ile Arg Trp Lys Gly Leu Pro Ile Thr Cys Lys Lys
      130      135      140
Asp Val Glu Glu Val Lys Met Asp Arg Asn Lys Val Met Ser Ser Val
      145      150      155      160
Gln Lys Lys Ala Ala Phe Leu Lys Glu Leu Arg Glu Lys Val Ser Ser
      165      170      175
Leu Glu Ser Leu Met Ser Arg Asn Gln Glu Met Val Val Lys Thr Gln
      180      185      190
Gly Pro Ala Glu Gly Phe Thr Leu Pro Phe Ile Leu Leu Glu Thr Asn
      195      200      205
Pro His Ala Val Val Glu Ile Glu Ile Ser Glu Asp Met Gln Leu Val
      210      215      220
His Leu Asp Phe Asn Ser Thr Pro Phe Ser Val His Asp Asp Ala Tyr
      225      230      235      240
Ile Leu Lys Leu Met Gln Glu Gln Lys Gln Glu Gln Asn Arg Val Ser
      245      250      255
Ser Ser Ser Ser Thr His His Gln Ser Gln His Ser Ser Ala His Ser
      260      265      270
Ser Ser Ser Ser Cys Ile Ala Ser Gly Thr Ser Gly Pro Val Cys Trp
      275      280      285
Asn Ser Gly Ser Ile Asp Thr Arg'
      290      295

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<210> 83

<211> 173

<212> PRT

<213> Arabidopsis thaliana

<400> 83

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Met Gln Pro Thr Glu Thr Ser Gln Pro Ala Pro Ser Asp Gln Gly Arg
1      5      10      15
Arg Leu Lys Asp Gln Leu Ser Glu Ser Met Ser Phe Ser Ser Gln Met
      20      25      30
Lys Lys Glu Asp Asp Glu Leu Ser Met Lys Ala Leu Ser Ala Phe Lys
      35      40      45
Ala Lys Glu Glu Glu Ile Glu Lys Lys Lys Met Glu Ile Arg Glu Arg
      50      55      60

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Val Gln Ala Gln Leu Gly Arg Val Glu Asp Glu Ser Lys Arg Leu Ala
 65 70 75 80
 Met Ile Arg Glu Glu Leu Glu Gly Phe Ala Asp Pro Met Arg Lys Glu
 85 90 95
 Val Thr Met Val Arg Lys Lys Ile Asp Ser Leu Asp Lys Glu Leu Lys
 100 105 110
 Pro Leu Gly Asn Thr Val Gln Lys Lys Glu Thr Glu Tyr Lys Asp Ala
 115 120 125
 Leu Glu Ala Phe Asn Glu Lys Asn Lys Glu Lys Val Glu Leu Ile Thr
 130 135 140
 Lys Leu Gln Glu Leu Glu Gly Glu Ser Glu Lys Phe Arg Phe Lys Lys
 145 150 155 160
 Leu Glu Glu Leu Ser Lys Asn Ile Asp Leu Thr Lys Pro
 165 170

<210> 84
 <211> 46
 <212> PRT
 <213> Arabidopsis thaliana

<400> 84
 Gln Lys Gln Ala Pro Gly Ala Gly Asp Val Pro Ala Thr Ile Gln Glu
 1 5 10 15
 Glu Asp Asp Asp Asp Asp Val Pro Asp Leu Val Val Gly Glu Thr Phe
 20 25 30
 Glu Thr Pro Ala Thr Glu Glu Ala Pro Lys Ala Ala Ser
 35 40 45

<210> 85
 <211> 383
 <212> PRT
 <213> Arabidopsis thaliana

<400> 85
 Met Glu Asp Asp Asp Glu Ile Gln Ser Ile Pro Ser Pro Gly Asp Ser
 1 5 10 15
 Ser Leu Ser Pro Gln Ala Pro Pro Ser Pro Pro Ile Leu Pro Thr Asn
 20 25 30
 Asp Val Thr Val Ala Val Val Lys Lys Pro Gln Pro Gly Leu Ser Ser
 35 40 45
 Gln Ser Pro Ser Met Asn Ala Leu Ala Leu Val Val His Thr Pro Ser
 50 55 60
 Val Thr Gly Gly Gly Gly Ser Gly Asn Arg Asn Gly Arg Gly Gly Gly
 65 70 75 80
 Gly Gly Ser Gly Gly Gly Gly Gly Gly Arg Asp Asp Cys Trp Ser Glu
 85 90 95
 Glu Ala Thr Lys Val Leu Ile Glu Ala Trp Gly Asp Arg Phe Ser Glu
 100 105 110
 Pro Gly Lys Gly Thr Leu Lys Gln Gln His Trp Lys Glu Val Ala Glu
 115 120 125
 Ile Val Asn Lys Ser Arg Gln Cys Lys Tyr Pro Lys Thr Asp Ile Gln
 130 135 140
 Cys Lys Asn Arg Ile Asp Thr Val Lys Lys Lys Tyr Lys Gln Glu Lys
 145 150 155 160
 Ala Lys Ile Ala Ser Gly Asp Gly Pro Ser Lys Trp Val Phe Phe Lys

				165				170					175		
Lys	Leu	Glu	Ser	180	Leu	Ile	Gly	Gly	Thr	Thr	Phe	Ile	Ala	Ser	Ser
Lys	Ala	Ser	Glu	195	Lys	Ala	Pro	Met	Gly	Gly	Ala	Leu	Gly	Asn	Arg
Ser	Ser	Met	Phe	210	Lys	Arg	Gln	Thr	Lys	Gly	Asn	Gln	Ile	Val	Gln
Gln	Gln	Glu	Lys	225	Arg	Gly	Ser	Asp	Ser	Met	Arg	Trp	His	Phe	Lys
Arg	Ser	Ala	Ser	245	Glu	Thr	Glu	Ser	Glu	Ser	Asp	Pro	Glu	Pro	Ala
Ser	Pro	Glu	Glu	260	Ser	Ala	Glu	Ser	Leu	Pro	Pro	Leu	Gln	Pro	Gln
Pro	Leu	Ser	Phe	275	His	Met	Pro	Lys	Arg	Leu	Lys	Val	Asp	Lys	Gly
Gly	Gly	Gly	Ser	290	Gly	Val	Gly	Asp	Val	Ala	Arg	Ala	Ile	Leu	Phe
Thr	Glu	Ala	Tyr	305	Glu	Lys	Ala	Glu	Thr	Ala	Lys	Leu	Lys	Leu	Ala
Glu	Leu	Glu	Lys	325	Glu	Arg	Met	Lys	Phe	Ala	Lys	Glu	Met	Glu	Gln
Arg	Met	Gln	Phe	340	Leu	Lys	Thr	Gln	Leu	Glu	Ile	Thr	Gln	Asn	Gln
Glu	Glu	Glu	Glu	355	Arg	Ser	Arg	Gln	Arg	Gly	Glu	Arg	Arg	Ile	Asp
Asp	Asp	Asp	Asp	370	Arg	Asn	Gly	Lys	Asn	Asn	Gly	Asn	Val	Ser	Ser

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<210> 86
<211> 131
<212> PRT
<213> Arabidopsis thaliana
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<220>
<221>    VARIANT
<222>    70,118
<223>    Xaa = any amino acid
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[illegible]

130

<210> 87
 <211> 181
 <212> PRT
 <213> Arabidopsis thaliana

<400> 87
 Gln Ala His Asp Ser Arg Ile Ala Cys Phe Ala Leu Thr Gln Asp Gly
 1 5 10 15
 His Leu Leu Ala Thr Ala Ser Ser Lys Gly Thr Leu Val Arg Ile Phe
 20 25 30
 Asn Thr Val Asp Gly Thr Leu Arg Gln Glu Val Arg Arg Gly Ala Asp
 35 40 45
 Arg Ala Glu Ile Tyr Ser Leu Ala Phe Ser Ser Asn Ala Gln Trp Leu
 50 55 60
 Ala Val Ser Ser Asp Lys Gly Thr Val His Val Phe Gly Leu Lys Val
 65 70 75 80
 Asn Ser Gly Ser Gln Val Lys Asp Ser Ser Arg Ile Ala Pro Asp Ala
 85 90 95
 Thr Pro Ser Ser Pro Ser Ser Ser Leu Ser Leu Phe Lys Gly Val Leu
 100 105 110
 Pro Arg Tyr Phe Ser Ser Glu Trp Ser Val Ala Gln Phe Arg Leu Val
 115 120 125
 Glu Gly Thr Gln Tyr Ile Ala Ala Phe Gly His Gln Lys Asn Thr Val
 130 135 140
 Val Ile Leu Gly Met Asp Gly Ser Phe Tyr Arg Cys Gln Phe Asp Pro
 145 150 155 160
 Val Asn Gly Gly Glu Met Ser Gln Leu Glu Tyr His Asn Cys Leu Lys
 165 170 175
 Pro Pro Ser Val Phe
 180

<210> 88
 <211> 175
 <212> PRT
 <213> Arabidopsis thaliana

<400> 88
 Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Lys Asp Pro
 1 5 10 15
 Lys Glu Phe Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser
 20 25 30
 Trp Arg Leu Asp Ala Asp Asn Tyr Glu Thr Asp Glu Asp Leu Lys Lys
 35 40 45
 Ile Arg Glu Ser Arg Gly Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys
 50 55 60
 Pro Glu Lys Leu Pro Asn Tyr Glu Val Lys Val Lys Ser Phe Phe Glu
 65 70 75 80
 Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Val Ala Gly Thr
 85 90 95
 Gly Tyr Phe Asp Val Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Leu
 100 105 110
 Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg
 115 120 125

Phe Thr Val Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe Val
 130 135 140
 Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro
 145 150 155 160
 Ala Arg Lys Glu Tyr Val Asp Asn Phe Met Ile Asn Ala Ser Ala
 165 170 175

<210> 89
 <211> 98
 <212> PRT
 <213> Arabidopsis thaliana

<400> 89
 Thr Ser Phe Pro Ile Thr Arg Lys Lys Thr Leu Lys Met Asp Gly His
 1 5 10 15
 Asp Ser Glu Asp Thr Lys Gln Ser Thr Ala Asp Met Thr Ala Phe Val
 20 25 30
 Gln Asn Leu Leu Gln Gln Met Gln Thr Arg Phe Gln Thr Met Ser Asp
 35 40 45
 Ser Ile Ile Thr Lys Ile Asp Asp Met Gly Gly Arg Ile Asn Glu Leu
 50 55 60
 Glu Gln Ser Ile Asn Asp Leu Arg Ala Glu Met Gly Val Glu Gly Thr
 65 70 75 80
 Pro Pro Pro Ala Ser Lys Ser Gly Asp Glu Pro Lys Thr Pro Ala Ser
 85 90 95
 Ser Ser

<210> 90
 <211> 117
 <212> PRT
 <213> Arabidopsis thaliana

<400> 90
 Ala Gln Val Arg Ala Lys Met Leu Lys Glu Val Ala Thr Glu Lys Gln
 1 5 10 15
 Thr Ala Val Asp Thr His Phe Ala Thr Ala Lys Lys Leu Ala Gln Glu
 20 25 30
 Gly Asp Ala Leu Phe Val Lys Ile Phe Ala Ile Lys Lys Leu Leu Ala
 35 40 45
 Lys Leu Glu Ala Glu Lys Glu Ser Val Asp Gly Lys Phe Lys Glu Thr
 50 55 60
 Val Lys Glu Leu Ser His Leu Leu Ala Asp Ala Ser Glu Ala Tyr Glu
 65 70 75 80
 Glu Tyr His Gly Ala Val Arg Lys Ala Lys Asp Glu Gln Ala Ala Glu
 85 90 95
 Glu Phe Ala Lys Glu Ala Thr Gln Ser Ala Glu Ile Ile Trp Val Lys
 100 105 110
 Phe Leu Ser Ser Leu
 115

<210> 91
 <211> 216
 <212> PRT

<213> Arabidopsis thaliana

<400> 91

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Met Glu Phe Gly Ser Phe Leu Val Ser Leu Gly Thr Ser Phe Val Ile
1      5      10      15
Phe Val Ile Leu Met Leu Leu Phe Thr Trp Leu Ser Arg Lys Ser Gly
      20      25      30
Asn Ala Pro Ile Tyr Tyr Pro Asn Arg Ile Leu Lys Gly Leu Glu Pro
      35      40      45
Trp Glu Gly Thr Ser Leu Thr Arg Asn Pro Phe Ala Trp Met Arg Glu
      50      55      60
Ala Leu Thr Ser Ser Glu Gln Asp Val Val Asn Leu Ser Gly Val Asp
65      70      75      80
Thr Ala Val His Phe Val Phe Leu Ser Thr Val Leu Gly Ile Phe Ala
      85      90      95
Cys Ser Ser Leu Leu Leu Leu Pro Thr Leu Leu Pro Leu Ala Ala Thr
      100      105      110
Asp Asn Asn Ile Lys Asn Thr Lys Asn Ala Thr Asp Thr Thr Ser Lys
      115      120      125
Gly Thr Phe Ser Gln Leu Asp Asn Leu Ser Met Ala Asn Ile Thr Lys
      130      135      140
Lys Ser Ser Arg Leu Trp Ala Phe Leu Gly Ala Val Tyr Trp Ile Ser
145      150      155      160
Leu Val Thr Tyr Phe Phe Leu Trp Lys Ala Tyr Lys His Val Ser Ser
      165      170      175
Leu Arg Ala Gln Ala Leu Met Ser Ala Asp Val Lys Pro Glu Gln Phe
      180      185      190
Ala Ile Leu Val Arg Asp Met Pro Ala Pro Pro Asp Gly Arg Arg Gly
      195      200      205
Arg Glu Phe Gln Ile Tyr Glu Ser
      210      215

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<210> 92

<211> 328

<212> PRT

<213> Arabidopsis thaliana

<400> 92

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Val His Thr Pro Ala Gly Glu Leu Gln Arg Gln Ile Arg Ser Trp Leu
1      5      10      15
Ala Glu Ser Phe Glu Phe Leu Ser Val Thr Ala Asp Asp Val Ser Gly
      20      25      30
Val Thr Thr Gly Gln Leu Glu Leu Leu Ser Thr Ala Ile Met Asp Gly
      35      40      45
Trp Met Ala Gly Val Gly Ala Pro Val Pro Pro His Thr Asp Ala Leu
      50      55      60
Gly Gln Leu Val Ser Glu Tyr Ala Lys Arg Val Tyr Thr Ser Gln Met
65      70      75      80
Gln His Leu Lys Asp Ile Ala Gly Thr Leu Ala Ser Glu Glu Ala Glu
      85      90      95
Asp Ala Gly Gln Val Ala Lys Leu Arg Ser Ala Leu Glu Ser Val Asp
      100      105      110
His Lys Arg Arg Lys Ile Leu Gln Met Arg Ser Asp Ala Ala Leu
      115      120      125
Phe Thr Leu Glu Glu Gly Ser Ser Pro Val Gln Asn Pro Ser Thr Ala
      130      135      140

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Ala Glu Asp Ser Arg Leu Ala Ser Leu Ile Ser Leu Asp Ala Ile Leu
 145 150 155 160
 Lys Gln Val Lys Glu Ile Thr Arg Gln Ala Ser Val His Val Leu Ser
 165 170 175
 Lys Ser Lys Lys Lys Ala Leu Leu Glu Ser Leu Asp Glu Leu Asn Glu
 180 185 190
 Arg Met Pro Ser Leu Leu Asp Val Asp His Pro Cys Ala Gln Arg Glu
 195 200 205
 Ile Asp Thr Ala His Gln Leu Val Glu Thr Ile Pro Glu Gln Glu Asp
 210 215 220
 Asn Leu Gln Asp Glu Lys Arg Pro Ser Ile Asp Ser Ile Ser Ser Thr
 225 230 235 240
 Glu Thr Asp Val Ser Gln Trp Asn Val Leu Gln Phe Asn Thr Gly Gly
 245 250 255
 Ser Ser Ala Pro Phe Ile Ile Lys Cys Gly Ala Asn Ser Asn Ser Glu
 260 265 270
 Leu Val Ile Lys Ala Asp Ala Arg Ile Gln Glu Pro Lys Gly Gly Glu
 275 280 285
 Ile Val Arg Val Val Pro Arg Pro Ser Val Leu Glu Asn Met Ser Leu
 290 295 300
 Glu Glu Met Lys Gln Val Phe Gly Gln Leu Pro Glu Ala Leu Ser Ser
 305 310 315 320
 Leu Ala Leu Ala Arg Thr Ala Asp
 325

<210> 93
 <211> 79
 <212> PRT
 <213> Arabidopsis thaliana

<400> 93
 Thr Tyr Glu Arg Leu Pro Ile Glu Glu Glu Gln Gln Gln Glu Gln Pro
 1 5 10 15
 Leu Gln Leu Glu Asp Gly Lys Lys Gln Lys Glu Glu Asn Asp Asp Asn
 20 25 30
 Glu Ser Gly Asn Asn Gly Asn Glu Gly Ser Met Gln Pro Pro Met Tyr
 35 40 45
 Asn Met Pro Pro Asn Phe Ile Pro Asn Gly His Gln Met Ala Gln His
 50 55 60
 Asp Val Tyr Trp Gly Gly Pro Pro Pro Arg Ala Pro Pro Ser Tyr
 65 70 75

<210> 94
 <211> 150
 <212> PRT
 <213> Arabidopsis thaliana

<400> 94
 Ser Lys Ala Arg Val Leu Ala Ile Pro Asp Asp Leu Ala Asn Val Ser
 1 5 10 15
 Cys Gly Val Glu Gln Ile Glu Glu Leu Lys Gly Leu Asn Leu Val Glu
 20 25 30
 Lys Asp Gly Gly Ser Ser Ser Ser Asp Gly Ala Arg Asn Thr Asn Pro
 35 40 45
 Glu Thr Arg Arg Tyr Ser Gly Ser Leu Gly Val Glu Asp Gly Ala Tyr

50		55		60
Thr Asn Glu Met Leu Gln Ser Ile Glu Met Val Thr Asp Val Leu Asp				
65		70		75
Ser Leu Val Arg Arg Val Thr Val Ala Glu Ser Glu Ser Ala Val Gln				80
	85		90	95
Lys Glu Arg Ala Leu Leu Gly Glu Glu Ile Ser Arg Lys Thr Ile				
	100		105	110
Gln Ile Glu Asn Leu Ser Val Lys Leu Glu Glu Met Glu Arg Phe Ala				
	115		120	125
Tyr Gly Thr Asn Ser Val Leu Asn Glu Met Arg Glu Arg Ile Glu Glu				
	130		135	140
Leu Val Glu Glu Thr Met				
145		150		

<210> 95
 <211> 181
 <212> PRT
 <213> Arabidopsis thaliana

<400> 95

Met Thr Asn Ile Ala Met Ala Asp Ala Leu Lys Ser Leu Glu Ile Val				
1	5		10	15
Asp Gly Leu Asp Glu Tyr Met Asn Gln Ser Glu Ser Ser Ala Pro His				
	20		25	30
Ser Pro Thr Ser Val Ala Lys Leu Pro Pro Ser Thr Ala Thr Arg Thr				
	35		40	45
Thr Arg Arg Lys Thr Thr Thr Lys Ala Glu Pro Gln Pro Ser Ser Gln				
	50		55	60
Leu Val Ser Arg Ser Cys Arg Ser Thr Ser Lys Ser Leu Ala Gly Asp				
65	70		75	80
Met Asp Gln Glu Asn Ile Asn Lys Asn Val Ala Gln Glu Met Lys Thr				
	85		90	95
Ser Asn Val Lys Phe Glu Ala Asn Val Leu Lys Thr Pro Ala Ala Gly				
	100		105	110
Ser Thr Arg Lys Thr Ser Ala Ala Thr Ser Cys Thr Lys Lys Asp Glu				
	115		120	125
Leu Val Gln Ser Val Tyr Ser Thr Arg Arg Ser Thr Arg Leu Leu Glu				
	130		135	140
Lys Cys Met Ala Asp Leu Ser Leu Lys Thr Lys Glu Thr Val Asp Asn				
145	150		155	160
Lys Pro Ala Lys Asn Glu Asp Thr Glu Gln Lys Val Ser Ala Gln Glu				
	165		170	175
Lys Asn Leu Thr Gly				
180				

<210> 96
 <211> 163
 <212> PRT
 <213> Arabidopsis thaliana

<400> 96

Met Leu Met Leu Cys Gly Phe Thr Val Leu Asp Met Leu Lys His His				
1	5		10	15
Asp Leu Gly Lys Ile Arg Ala Pro Leu His Pro Leu Arg Lys Lys Met				
	20		25	30

Gln Ile Gln His Ala Tyr Gln Gln Ile His Gln Gly Ser Lys Leu Leu
 35 40 45
 Lys Met Asp Arg Met Met Leu Arg Gly Thr Lys Arg Arg Ile Gly Val
 50 55 60
 Arg Lys Gly Asn Leu Gln Arg Glu Arg Arg Lys Lys Asp Met Ile Gly
 65 70 75 80
 Val Lys Asn Ala Lys Gly Met Arg Ser Glu Ala Leu Val Ile Gln Met
 85 90 95
 Ile Glu Arg Ser Thr Arg Lys Arg Arg Arg Lys Lys Glu Gly Met
 100 105 110
 Thr Leu Ile Leu Ile Glu Ala Asn Cys Pro Arg Met Glu His Phe Ala
 115 120 125
 Leu Gln Arg Lys Ser Gly Arg Leu Gly Thr Lys Ile Gln Leu Pro Leu
 130 135 140
 Leu Gln Asp Leu Asn Leu Leu Leu Ile Ser Phe Thr Asn Arg Gly Val
 145 150 155 160
 Lys Cys Cys

<210> 97
 <211> 170
 <212> PRT
 <213> Arabidopsis thaliana

<400> 97
 Gly Thr Arg Gln Lys Arg Glu Thr Ser Asp Pro Glu Ser Asp Leu Lys
 1 5 10 15
 Thr Arg Lys Asn Arg Lys Met Gly Lys Asp Gly Leu Ser Asp Asp Gln
 20 25 30
 Val Ser Ser Met Lys Glu Ala Phe Met Leu Phe Asp Thr Asp Gly Asp
 35 40 45
 Gly Lys Ile Ala Pro Ser Glu Leu Gly Ile Leu Met Arg Ser Leu Gly
 50 55 60
 Gly Asn Pro Thr Gln Ala Gln Leu Lys Ser Ile Ile Ala Ser Glu Asn
 65 70 75 80
 Leu Ser Ser Pro Phe Asp Phe Asn Arg Phe Leu Asp Leu Met Ala Lys
 85 90 95
 His Leu Lys Thr Glu Pro Phe Asp Arg Gln Leu Arg Asp Ala Phe Lys
 100 105 110
 Val Leu Asp Lys Glu Gly Thr Gly Phe Val Ala Val Ala Asp Leu Arg
 115 120 125
 His Ile Leu Thr Ser Ile Gly Glu Lys Leu Glu Pro Asn Glu Phe Asp
 130 135 140
 Glu Trp Ile Lys Glu Val Asp Val Gly Ser Asp Gly Lys Ile Arg Tyr
 145 150 155 160
 Glu Asp Phe Ile Ala Arg Met Val Ala Lys
 165 170

<210> 98
 <211> 38
 <212> PRT
 <213> Arabidopsis thaliana

<400> 98
 Arg Gly Val Ser Phe Arg Ser Arg Glu Met Arg Pro Ile Phe Ala Ile

<400>	99															
Met 1	Thr	Thr	Thr	Gly 5	Ser	Asn	Ser	Asn	His 10	Asn	His	His	Glu	Ser 15	Asn	
Asn	Asn	Asn	Asn	Asn 20	Pro	Ser	Thr	Arg 25	Ser	Trp	Gly	Thr	Ala 30	Val	Ser	
Gly	Gln	Ser	Val	Ser 35	Thr	Ser	Gly 40	Ser	Met	Gly	Ser	Pro 45	Ser	Ser	Arg	
Ser	Glu	Gln	Thr	Ile 50	Thr	Val	Val 55	Thr	Ser	Thr	Ser	Asp 60	Thr	Thr	Phe	
Gln 65	Arg	Leu	Asn	Asn 70	Leu	Asp	Ile	Gln	Gly	Asp 75	Asp	Ala	Gly	Ser	Gln 80	
Gly	Ala	Ser	Gly	Val 85	Lys	Lys	Lys	Lys	Arg 90	Gly	Gln	Arg	Ala 95	Ala	Gly	
Pro	Asp	Lys	Thr	Gly 100	Arg	Gly	Leu	Arg 105	Gln	Phe	Ser	Met	Lys 110	Val	Cys	
Glu	Lys	Val	Glu	Ser 115	Lys	Gly	Arg	Thr 120	Thr	Tyr	Asn	Glu	Val 125	Ala	Asp	
Glu	Leu	Val	Ala	Glu 130	Phe	Ala	Leu 135	Pro	Asn	Asn	Asp	Gly	Thr	Ser	Pro	
Asp 145	Gln	Gln	Gln	Tyr 150	Asp	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Val	Tyr	Asp	
Ala	Leu	Asn	Val	Leu 165	Met	Ala	Met	Asp	Ile 170	Ile	Ser	Lys	Asp	Lys	Lys	
Glu	Ile	Gln	Trp	Arg 180	Gly	Leu	Pro	Arg	Thr 185	Ser	Leu	Ser	Asp	Ile	Glu	
Glu	Leu	Lys	Asn	Glu 195	Arg	Leu	Ser	Leu	Arg	Asn	Arg	Ile	Glu	Lys	Lys	
Thr	Ala	Tyr	Ser	Gln 210	Glu	Leu	Glu	Glu	Gln	Arg	Asn	Glu	His	Leu	Tyr	
Ser 225	Ser	Gly	Asn	Ala 230	Pro	Ser	Gly	Gly	Val	Ala	Leu	Pro	Phe	Ile	Leu	
Val	Gln	Thr	Arg	Pro 245	His	Ala	Thr	Val	Glu	Val	Glu	Ile	Ser	Glu	Asp	
Met	Gln	Leu	Val	His 260	Phe	Asp	Phe	Asn	Ser	Thr	Pro	Phe	Glu	Leu	His	
Asp	Asp	Asn	Phe	Val 275	Leu	Lys	Thr	Met	Lys	Phe	Cys	Asp	Gln	Pro	Pro	
Gln	Gln	Pro	Asn	Gly 290	Arg	Asn	Asn	Ser	Gln	Leu	Val	Cys	His	Asn	Phe	
Thr 305	Pro	Glu	Asn	Pro 310	Asn	Lys	Gly	Pro	Ser	Thr	Gly	Pro	Thr	Pro	Gln	
Leu	Asp	Met	Tyr	Glu 325	Thr	His	Leu	Gln	Ser	Gln	Gln	His	Gln	Gln	His	
Ser	Gln	Leu	Gln	Ile 340	Ile	Pro	Met	Pro	Glu	Thr	Asn	Asn	Val	Thr	Ser	

Ser Ala Asp Thr Ala Pro Val Lys Ser Pro Ser Leu Pro Gly Ile Met
 355 360 365
 Asn Ser Ser Met Lys Pro Glu Asn
 370 375

<210> 100
 <211> 145
 <212> PRT
 <213> Arabidopsis thaliana

<400> 100
 Glu Tyr Leu Lys Lys Gly Ser Pro Ile Ser Ala Leu Lys Ser Phe Ile
 1 5 10 15
 Ser Ser Leu Ser Glu Pro Pro Gln Asp Ile Met Asp Ala Leu Phe Asn
 20 25 30
 Ala Leu Phe Asp Gly Val Gly Lys Gly Phe Ala Lys Glu Val Thr Lys
 35 40 45
 Lys Lys Asn Tyr Leu Ala Ala Ala Thr Met Gln Glu Asp Gly Ser
 50 55 60
 Gln Met His Leu Leu Asn Ser Ile Gly Thr Phe Cys Gly Lys Asn Gly
 65 70 75 80
 Asn Glu Glu Ala Leu Lys Glu Val Ala Leu Val Leu Lys Ala Leu Tyr
 85 90 95
 Asp Gln Asp Ile Ile Glu Glu Glu Val Val Leu Asp Trp Tyr Glu Lys
 100 105 110
 Gly Leu Thr Gly Ala Asp Lys Ser Ser Pro Val Trp Lys Asn Val Lys
 115 120 125
 Pro Phe Val Glu Trp Leu Gln Ser Ala Glu Ser Glu Ser Glu Glu Glu
 130 135 140
 Asp
 145

<210> 101
 <211> 316
 <212> PRT
 <213> Arabidopsis thaliana

<400> 101
 Leu Glu Val Glu Arg Asn Ala Ser Ala Val Ala Ala Ser Glu Thr Met
 1 5 10 15
 Ala Met Ile Asn Arg Leu His Glu Glu Lys Ala Ala Met Gln Met Glu
 20 25 30
 Ala Leu Gln Tyr Gln Arg Met Met Glu Glu Gln Ala Glu Phe Asp Gln
 35 40 45
 Glu Ala Leu Gln Leu Leu Asn Glu Leu Met Val Asn Arg Glu Lys Glu
 50 55 60
 Asn Ala Glu Leu Glu Lys Glu Leu Glu Val Tyr Arg Lys Arg Met Glu
 65 70 75 80
 Glu Tyr Glu Ala Lys Glu Lys Met Gly Met Leu Arg Arg Arg Leu Arg
 85 90 95
 Asp Ser Ser Val Asp Ser Tyr Arg Asn Asn Gly Asp Ser Asp Glu Asn
 100 105 110
 Ser Asn Gly Glu Leu Gln Phe Lys Asn Val Glu Gly Val Thr Asp Trp
 115 120 125
 Lys Tyr Arg Glu Asn Glu Met Glu Asn Thr Pro Val Asp Val Val Leu

130		135		140
Arg Leu Asp Glu Cys Leu	Asp Asp Tyr Asp Gly	Glu Arg Leu Ser Ile		
145		150		160
Leu Gly Arg Leu Lys Phe	Leu Glu Glu Lys Leu	Thr Asp Leu Asn Asn		
	165	170		175
Glu Glu Asp Asp Glu Glu	Ala Lys Thr Phe Glu	Ser Asn Gly Ser		
	180	185		190
Ile Asn Gly Asn Glu His	Ile His Gly Lys Glu	Thr Asn Gly Lys His		
	195	200		205
Arg Val Ile Gln Ser Lys	Arg Leu Leu Pro Leu	Phe Asp Ala Val Asp		
	210	215		220
Gly Glu Met Glu Asn Gly	Leu Ser Asn Gly Asn	His His Glu Asn Gly		
225		230		240
Phe Asp Asp Ser Glu Lys	Gly Glu Asn Val Thr	Ile Glu Glu Glu Val		
	245	250		255
Asp Glu Leu Tyr Glu Arg	Leu Glu Ala Leu Glu	Ala Asp Arg Glu Phe		
	260	265		270
Leu Arg His Cys Val Gly	Ser Leu Lys Lys Gly	Asp Lys Gly Val His		
	275	280		285
Leu Leu His Glu Ile Leu	Gln His Leu Arg Asp	Leu Arg Asn Ile Asp		
	290	295		300
Leu Thr Arg Val Arg Glu	Asn Gly Asp Met Ser	Leu		
305		310		315

<210> 102
 <211> 194
 <212> PRT
 <213> Arabidopsis thaliana

<400> 102
 Ala Ser Leu Ile Lys Leu Ile Arg Leu Leu Glu Thr Pro Ile Phe Thr
 1 5 10 15
 Tyr Leu Arg Leu Gln Leu Leu Glu Pro Gly Arg Tyr Thr Trp Leu Leu
 20 25 30
 Lys Thr Leu Tyr Gly Leu Leu Met Leu Leu Pro Gln Gln Ser Ala Ala
 35 40 45
 Phe Lys Ile Leu Arg Thr Arg Leu Lys Thr Val Pro Thr Tyr Ser Phe
 50 55 60
 Ser Thr Gly Asn Gln Ile Gly Arg Ala Thr Ser Gly Val Pro Phe Ser
 65 70 75 80
 Gln Tyr Lys His Gln Asn Glu Asp Gly Asp Leu Glu Asp Asp Asn Ile
 85 90 95
 Asn Ser Ser His Gln Gly Ile Asn Phe Ala Val Arg Leu Gln Gln Phe
 100 105 110
 Glu Asn Val Gln Asn Leu His Arg Gly Gln Ala Arg Thr Arg Val Asn
 115 120 125
 Tyr Ser Tyr His Ser Ser Ser Ser Ser Thr Ser Lys Glu Val Arg Arg
 130 135 140
 Ser Glu Glu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 145 150 155 160
 Gln Gln Gln Arg Pro Pro Pro Ser Ser Thr Ser Ser Ser Val Ala Asp
 165 170 175
 Asn Asn Arg Pro Pro Ser Arg Thr Ser Arg Lys Gly Pro Gly Gln Leu
 180 185 190
 Gln Leu

<210> 103
 <211> 289
 <212> PRT
 <213> Arabidopsis thaliana

<400> 103
 Leu Ile Glu Thr Ser Val Glu Ser Lys Glu Thr Thr Glu Ser Val Val
 1 5 10 15
 Thr Gly Glu Ser Glu Lys Ala Ile Glu Asp Ile Ser Lys Glu Ala Asp
 20 25 30
 Asn Glu Glu Asp Asp Asp Glu Glu Glu Gln Glu Gly Asp Glu Asp Asp
 35 40 45
 Asp Glu Asn Glu Glu Glu Glu Val Val Val Pro Glu Thr Glu Asn Arg
 50 55 60
 Ala Glu Gly Glu Asp Leu Val Lys Asn Lys Ala Ala Asp Ala Lys Lys
 65 70 75 80
 His Leu Gln Met Ile Gly Val Gln Leu Leu Lys Glu Ser Asp Glu Ala
 85 90 95
 Asn Arg Thr Lys Lys Arg Gly Lys Arg Ala Ser Arg Met Thr Leu Glu
 100 105 110
 Asp Asp Ala Asp Glu Asp Trp Phe Pro Glu Glu Pro Phe Glu Ala Phe
 115 120 125
 Lys Glu Met Arg Glu Arg Lys Val Phe Asp Val Ala Asp Met Tyr Thr
 130 135 140
 Ile Ala Asp Val Trp Gly Trp Thr Trp Glu Lys Asp Phe Lys Asn Lys
 145 150 155 160
 Thr Pro Arg Lys Trp Ser Gln Glu Trp Glu Val Glu Leu Ala Ile Val
 165 170 175
 Leu Met Thr Lys Val Ile Glu Leu Gly Gly Ile Pro Thr Ile Gly Asp
 180 185 190
 Cys Ala Val Ile Leu Arg Ala Ala Leu Arg Ala Pro Met Pro Ser Ala
 195 200 205
 Phe Leu Lys Ile Leu Gln Thr Thr His Ser Leu Gly Tyr Ser Phe Gly
 210 215 220
 Ser Pro Leu Tyr Asp Glu Ile Ile Thr Leu Cys Leu Asp Leu Gly Glu
 225 230 235 240
 Leu Asp Ala Ala Ile Ala Ile Val Ala Asp Met Glu Thr Thr Gly Ile
 245 250 255
 Thr Val Pro Asp Gln Thr Leu Asp Lys Val Ile Ser Ala Arg Gln Ser
 260 265 270
 Asn Glu Ser Pro Arg Ser Glu Pro Glu Glu Pro Ala Ser Thr Val Ser
 275 280 285
 Ser

<210> 104
 <211> 333
 <212> PRT
 <213> Arabidopsis thaliana

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 Thr Asp Ser Ala Ser Asp Ser Ile Phe His Tyr Asp Asp Ala Ser Gln
 1 5 10 15
 Ala Lys Ile Gln Gln Glu Lys Pro Trp Ala Ser Asp Pro Asn Tyr Phe

			20					25					30			
Lys	Arg	Val	His	Ile	Ser	Ala	Leu	Ala	Leu	Leu	Lys	Met	Val	Val	His	
		35					40					45				
Ala	Arg	Ser	Gly	Gly	Thr	Ile	Glu	Ile	Met	Gly	Leu	Met	Gln	Gly	Lys	
	50					55					60					
Thr	Glu	Gly	Asp	Thr	Ile	Ile	Val	Met	Asp	Ala	Phe	Ala	Leu	Pro	Val	
65				70					75						80	
Glu	Gly	Thr	Glu	Thr	Arg	Val	Asn	Ala	Gln	Ser	Asp	Ala	Tyr	Glu	Tyr	
			85					90						95		
Met	Val	Glu	Tyr	Ser	Gln	Thr	Ser	Lys	Leu	Ala	Gly	Arg	Leu	Glu	Asn	
		100						105					110			
Val	Val	Gly	Trp	Tyr	His	Ser	His	Pro	Gly	Tyr	Gly	Cys	Trp	Leu	Ser	
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Gly	Ile	Asp	Val	Ser	Thr	Gln	Met	Leu	Asn	Gln	Gln	Tyr	Gln	Glu	Pro	
	130					135					140					
Phe	Leu	Ala	Val	Val	Ile	Asp	Pro	Thr	Arg	Thr	Val	Ser	Ala	Gly	Lys	
145					150					155					160	
Val	Glu	Ile	Gly	Ala	Phe	Arg	Thr	Tyr	Pro	Glu	Gly	His	Lys	Ile	Ser	
			165					170						175		
Asp	Asp	His	Val	Ser	Glu	Tyr	Gln	Thr	Ile	Pro	Leu	Asn	Lys	Ile	Glu	
		180						185					190			
Asp	Phe	Gly	Val	His	Cys	Lys	Gln	Tyr	Tyr	Ser	Leu	Asp	Ile	Thr	Tyr	
		195					200					205				
Phe	Lys	Ser	Ser	Leu	Asp	Ser	His	Leu	Leu	Asp	Leu	Leu	Trp	Asn	Lys	
	210					215					220					
Tyr	Trp	Val	Asn	Thr	Leu	Ser	Ser	Ser	Pro	Leu	Leu	Gly	Asn	Gly	Asp	
225				230						235				240		
Tyr	Val	Ala	Gly	Gln	Ile	Ser	Asp	Leu	Ala	Glu	Lys	Leu	Glu	Gln	Ala	
			245					250						255		
Glu	Ser	Gln	Leu	Ala	Asn	Ser	Arg	Tyr	Gly	Gly	Ile	Ala	Pro	Ala	Gly	
		260						265					270			
His	Gln	Arg	Arg	Lys	Glu	Asp	Glu	Pro	Gln	Leu	Ala	Lys	Ile	Thr	Arg	
		275					280					285				
Asp	Ser	Ala	Lys	Ile	Thr	Val	Glu	Gln	Val	His	Gly	Leu	Met	Ser	Gln	
	290					295					300					
Val	Ile	Lys	Asp	Ile	Leu	Phe	Asn	Ser	Ala	Arg	Gln	Ser	Lys	Lys	Ser	
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Ala	Asp	Asp	Ser	Ser	Asp	Pro	Glu	Pro	Met	Ile	Thr	Ser				
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<210> 105
<211> 460
<212> PRT
<213> Arabidopsis thaliana
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			20					25					30		
Phe	Val	Leu	Phe	Asp	Phe	Ser	Pro	Lys	Leu	Ile	Leu	Asn	Leu	Leu	Asp
		35				40						45			
Val	Gly	Gly	Gly	Val	Val	Gly	Lys	Ile	Lys	Thr	Thr	Ala	Thr	Thr	Gly
	50					55					60				
Pro	Thr	Arg	Arg	Ala	Leu	Ser	Thr	Ile	Asn	Lys	Asn	Ile	Thr	Glu	Ala
65					70					75					80

Pro	Ser	Tyr	Pro	Tyr	Ala	Val	Asn	Lys	Arg	Ser	Val	Ser	Glu	Arg	Asp
				85					90					95	
Gly	Ile	Cys	Asn	Lys	Pro	Pro	Val	His	Arg	Pro	Val	Thr	Arg	Lys	Phe
			100					105					110		
Ala	Ala	Gln	Leu	Ala	Asp	His	Lys	Pro	His	Ile	Arg	Asp	Glu	Glu	Thr
		115					120					125			
Lys	Lys	Pro	Asp	Ser	Val	Ser	Ser	Glu	Glu	Pro	Glu	Thr	Ile	Ile	Ile
	130					135					140				
Asp	Val	Asp	Glu	Ser	Asp	Lys	Glu	Gly	Gly	Asp	Ser	Asn	Glu	Pro	Met
145					150					155					160
Phe	Val	Gln	His	Thr	Glu	Ala	Met	Leu	Glu	Glu	Ile	Glu	Gln	Met	Glu
				165					170					175	
Lys	Glu	Ile	Glu	Met	Glu	Asp	Ala	Asp	Lys	Glu	Glu	Glu	Pro	Val	Ile
			180					185					190		
Asp	Ile	Asp	Ala	Cys	Asp	Lys	Asn	Asn	Pro	Leu	Ala	Ala	Val	Glu	Tyr
		195					200					205			
Ile	His	Asp	Met	His	Thr	Phe	Tyr	Lys	Asn	Phe	Glu	Lys	Leu	Ser	Cys
	210					215					220				
Val	Pro	Pro	Asn	Tyr	Met	Asp	Asn	Gln	Gln	Asp	Leu	Asn	Glu	Arg	Met
225					230					235					240
Arg	Gly	Ile	Leu	Ile	Asp	Trp	Leu	Ile	Glu	Val	His	Tyr	Lys	Phe	Glu
				245					250					255	
Leu	Met	Glu	Glu	Thr	Leu	Tyr	Leu	Thr	Ile	Asn	Val	Ile	Asp	Arg	Phe
			260					265					270		
Leu	Ala	Val	His	Gln	Ile	Val	Arg	Lys	Lys	Leu	Gln	Leu	Val	Gly	Val
		275					280					285			
Thr	Ala	Leu	Leu	Leu	Ala	Cys	Lys	Tyr	Glu	Glu	Val	Ser	Val	Pro	Val
	290					295					300				
Val	Asp	Asp	Leu	Ile	Leu	Ile	Ser	Asp	Lys	Ala	Tyr	Ser	Arg	Arg	Glu
305					310					315					320
Val	Leu	Asp	Met	Glu	Lys	Leu	Met	Ala	Asn	Thr	Leu	Gln	Phe	Asn	Phe
				325					330					335	
Ser	Leu	Pro	Thr	Pro	Tyr	Val	Phe	Met	Lys	Arg	Phe	Leu	Lys	Ala	Ala
			340					345					350		
Gln	Ser	Asp	Lys	Lys	Leu	Glu	Ile	Leu	Ser	Phe	Phe	Met	Ile	Glu	Leu
		355					360					365			
Cys	Leu	Val	Glu	Tyr	Glu	Met	Leu	Glu	Tyr	Leu	Pro	Ser	Lys	Leu	Ala
	370					375					380				
Ala	Ser	Ala	Ile	Tyr	Thr	Ala	Gln	Cys	Thr	Leu	Lys	Gly	Phe	Glu	Glu
385					390					395					400
Trp	Ser	Lys	Thr	Cys	Glu	Phe	His	Thr	Gly	Tyr	Asn	Glu	Lys	Gln	Leu
				405					410					415	
Leu	Ala	Cys	Ala	Arg	Lys	Met	Val	Ala	Phe	His	His	Lys	Ala	Gly	Thr
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Gly	Lys	Leu	Thr												

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<210> 106
<211> 664
<212> PRT
<213> Arabidopsis thaliana
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Val	Asp	Asp 35	Asp	Pro	Thr	Cys	Leu 40	Met	Ile	Leu	Glu	Arg 45	Met	Leu	Met	
Thr	Cys 50	Leu	Tyr	Arg	Val	Thr 55	Lys	Cys	Asn	Arg	Ala	Glu	Ser	Ala	Leu	
Ser 65	Leu	Leu	Arg	Lys 70	Asn	Lys	Asn	Gly	Phe	Asp 75	Ile	Val	Ile	Ser	Asp 80	
Val	His	Met	Pro	Asp 85	Met	Asp	Gly	Phe	Lys 90	Leu	Leu	Glu	His	Val 95	Gly	
Leu	Glu	Met	Asp 100	Leu	Pro	Val	Ile	Met 105	Met	Ser	Ala	Asp	Asp 110	Ser	Lys	
Ser	Val 115	Val	Leu	Lys	Gly	Val	Thr 120	His	Gly	Ala	Val	Asp 125	Tyr	Leu	Ile	
Lys 130	Pro	Val	Arg	Ile	Glu	Ala 135	Leu	Lys	Asn	Ile	Trp 140	Gln	His	Val	Val	
Arg 145	Lys	Lys	Arg	Asn 150	Glu	Trp	Asn	Val	Ser	Glu 155	His	Ser	Gly	Gly	Ser 160	
Ile	Glu	Asp	Thr 165	Gly	Gly	Asp	Arg	Asp	Arg 170	Gln	Gln	Gln	His	Arg 175	Glu	
Asp	Ala	Asp	Asn 180	Asn	Ser	Ser	Ser	Val 185	Asn	Glu	Gly	Asn 190	Gly	Arg	Ser	
Ser	Arg 195	Lys	Arg	Lys	Glu	Glu	Glu 200	Val	Asp	Asp	Gln	Gly 205	Asp	Asp	Lys	
Glu 210	Asp	Ser	Ser	Ser	Leu	Lys 215	Lys	Pro	Arg	Val	Val 220	Trp	Ser	Val	Glu	
Leu 225	His	Gln	Gln	Phe 230	Val	Ala	Ala	Val	Asn	Gln 235	Leu	Gly	Val	Asp	Lys 240	
Ala	Val	Pro	Lys 245	Lys	Ile	Leu	Glu	Met 250	Met	Asn	Val	Pro	Gly	Leu 255	Thr	
Arg	Glu	Asn 260	Val	Ala	Ser	His	Leu 265	Gln	Lys	Tyr	Arg	Ile 270	Tyr	Leu	Arg	
Arg	Leu 275	Gly	Gly	Val	Ser	Gln	His 280	Gln	Gly	Asn	Met 285	Asn	His	Ser	Phe	
Met	Thr 290	Gly	Gln	Asp	Gln	Ser 295	Phe	Gly	Pro	Leu	Ser 300	Ser	Leu	Asn	Gly	
Phe 305	Asp	Leu	Gln	Ser 310	Leu	Ala	Val	Thr	Gly	Gln 315	Leu	Pro	Pro	Gln	Ser 320	
Leu	Ala	Gln	Leu 325	Gln	Ala	Ala	Gly	Leu 330	Gly	Arg	Pro	Thr	Leu 335	Ala	Lys	
Pro	Gly 340	Met	Ser	Val	Ser	Pro	Leu 345	Val	Asp	Gln	Arg	Ser 350	Ile	Phe	Asn	
Phe	Glu 355	Asn	Pro	Lys	Ile	Arg	Phe 360	Gly	Asp	Gly	His 365	Gly	Gln	Thr	Met	
Asn 370	Asn	Gly	Asn	Leu	Leu	His 375	Gly	Val	Pro	Thr 380	Gly	Ser	His	Met	Arg	
Leu 385	Arg	Pro	Gly	Gln 390	Asn	Val	Gln	Ser	Ser	Gly 395	Met	Met	Leu	Pro	Val 400	
Ala	Asp	Gln	Leu 405	Pro	Arg	Gly	Gly	Pro 410	Ser	Met	Leu	Pro	Ser 415	Leu	Gly	
Gln	Gln 420	Pro	Ile	Leu	Ser	Ser	Ser 425	Val	Ser	Arg	Arg	Ser 430	Asp	Leu	Thr	
Gly	Ala 435	Leu	Ala	Val	Arg	Asn 440	Ser	Ile	Pro	Glu	Thr 445	Asn	Ser	Arg	Val	
Leu	Pro 450	Thr	Thr	His	Ser	Val 455	Phe	Asn	Asn	Phe 460	Pro	Ala	Asp	Leu	Pro	

Arg Ser Ser Phe Pro Leu Ala Ser Ala Pro Gly Ile Ser Val Pro Val
 465 470 475 480
 Ser Val Ser Tyr Gln Glu Glu Val Asn Ser Ser Asp Ala Lys Gly Gly
 485 490 495
 Ser Ser Ala Ala Thr Ala Gly Phe Gly Asn Pro Ser Tyr Asp Ile Phe
 500 505 510
 Asn Asp Phe Pro Gln His Gln Gln His Asn Lys Asn Ile Ser Asn Lys
 515 520 525
 Leu Asn Asp Trp Asp Leu Arg Asn Met Gly Leu Val Phe Ser Ser Asn
 530 535 540
 Gln Asp Ala Ala Thr Ala Thr Ala Thr Ala Ala Phe Ser Thr Ser Glu
 545 550 555 560
 Ala Tyr Ser Ser Ser Ser Thr Gln Arg Lys Arg Arg Glu Thr Asp Ala
 565 570 575
 Thr Val Val Gly Glu His Gly Gln Asn Leu Gln Ser Pro Ser Arg Asn
 580 585 590
 Leu Tyr His Leu Asn His Val Phe Met Asp Gly Gly Ser Val Arg Val
 595 600 605
 Lys Ser Glu Arg Val Ala Glu Thr Val Thr Cys Pro Pro Ala Asn Thr
 610 615 620
 Leu Phe His Glu Gln Tyr Asn Gln Glu Asp Leu Met Ser Ala Phe Leu
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 Tyr Ser Ile Asp Asn Ile Gln Val
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<210> 107
 <211> 450
 <212> PRT
 <213> Arabidopsis thaliana

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 35 40 45
 Pro Asn Lys Arg Lys Lys Arg Ala Val Leu Gly Glu Ile Thr Asn Val
 50 55 60
 Asn Ser Asn Thr Ala Ile Leu Glu Ala Lys Asn Ser Lys Gln Ile Lys
 65 70 75 80
 Lys Gly Arg Gly His Gly Leu Ala Ser Thr Ser Gln Leu Ala Thr Ser
 85 90 95
 Val Thr Ser Glu Val Thr Asp Leu Gln Ser Arg Thr Asp Ala Lys Val
 100 105 110
 Glu Val Ala Ser Asn Thr Ala Gly Asn Leu Ser Val Ser Lys Gly Thr
 115 120 125
 Asp Asn Thr Ala Asp Asn Cys Ile Glu Ile Trp Asn Ser Arg Leu Pro
 130 135 140
 Pro Arg Pro Leu Gly Arg Ser Ala Ser Thr Ala Glu Lys Ser Ala Val
 145 150 155 160
 Ile Gly Ser Ser Thr Val Pro Asp Ile Pro Lys Phe Val Asp Ile Asp
 165 170 175
 Ser Asp Asp Lys Asp Pro Leu Leu Cys Cys Leu Tyr Ala Pro Glu Ile

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180      185      190
His Tyr Asn Leu Arg Val Ser Glu Leu Lys Arg Arg Pro Leu Pro Asp
195      200      205
Phe Met Glu Arg Ile Gln Lys Asp Val Thr Gln Ser Met Arg Gly Ile
210      215      220
Leu Val Asp Trp Leu Val Glu Val Ser Glu Glu Tyr Thr Leu Ala Ser
225      230      235
Asp Thr Leu Tyr Leu Thr Val Tyr Leu Ile Asp Trp Phe Leu His Gly
245      250      255
Asn Tyr Val Gln Arg Gln Gln Leu Gln Leu Leu Gly Ile Thr Cys Met
260      265      270
Leu Ile Ala Ser Lys Tyr Glu Glu Ile Ser Ala Pro Arg Ile Glu Glu
275      280      285
Phe Cys Phe Ile Thr Asp Asn Thr Tyr Thr Arg Asp Gln Val Leu Glu
290      295      300
Met Glu Asn Gln Val Leu Lys His Phe Ser Phe Gln Ile Tyr Thr Pro
305      310      315
Thr Pro Lys Thr Phe Leu Arg Arg Phe Leu Arg Ala Ala Gln Ala Ser
325      330      335
Arg Leu Ser Pro Ser Leu Glu Val Glu Phe Leu Ala Ser Tyr Leu Thr
340      345      350
Glu Leu Thr Leu Ile Asp Tyr His Phe Leu Lys Phe Leu Pro Ser Val
355      360      365
Val Ala Ala Ser Ala Val Phe Leu Ala Lys Trp Thr Met Asp Gln Ser
370      375      380
Asn His Pro Trp Asn Pro Thr Leu Glu His Tyr Thr Thr Tyr Lys Ala
385      390      395
Ser Asp Leu Lys Ala Ser Val His Ala Leu Gln Asp Leu Gln Leu Asn
405      410      415
Thr Lys Gly Cys Pro Leu Ser Ala Ile Arg Met Lys Tyr Arg Gln Glu
420      425      430
Lys Tyr Lys Ser Val Ala Val Leu Thr Ser Pro Lys Leu Leu Asp Thr
435      440      445
Leu Phe
450

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<210> 108
<211> 901
<212> PRT
<213> Arabidopsis thaliana

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<400> 108
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Asn Val Gln Ser Gln Pro Pro Gln Tyr Ser Gln Pro Ile Gln Gln Gln
35      40      45
Gln Leu Phe Pro Val Arg Pro Gly Gln Pro Val His Ile Thr Ser Ser
50      55      60
Ser Gln Ala Val Ser Val Pro Tyr Ile Gln Thr Asn Lys Ile Leu Thr
65      70      75      80
Ser Gly Ser Thr Gln Pro Gln Pro Asn Ala Pro Pro Met Thr Gly Phe
85      90      95
Ala Thr Ser Gly Pro Pro Phe Ser Ser Pro Tyr Thr Phe Val Pro Ser
100      105      110

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Ser	Tyr	Pro	Gln	Gln	Gln	Pro	Thr	Ser	Leu	Val	Gln	Pro	Asn	Ser	Gln
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		130					135					140			
Val	Asn	Gln	Ser	Thr	Ser	Leu	Val	Ser	Pro	Val	Gln	Gln	Thr	Gly	Gln
145							150				155				160
Gln	Thr	Pro	Val	Ala	Val	Ser	Thr	Asp	Pro	Gly	Asn	Leu	Thr	Pro	Gln
Ser	Ala	Ser	Asp	Trp	Gln	Glu	His	Thr	Ser	Ala	Asp	Gly	Arg	Lys	Ala
Asp	Ala	Ser	Thr	Val	Trp	Lys	Glu	Phe	Thr	Thr	Pro	Glu	Gly	Lys	Lys
Tyr	Tyr	Tyr	Asn	Lys	Val	Thr	Lys	Glu	Ser	Lys	Trp	Thr	Ile	Pro	Glu
Asp	Leu	Lys	Leu	Ala	Arg	Glu	Gln	Ala	Gln	Leu	Ala	Ser	Glu	Lys	Thr
225															240
Ser	Leu	Ser	Glu	Ala	Gly	Ser	Thr	Pro	Leu	Ser	His	His	Ala	Ala	Ser
Ser	Ser	Asp	Leu	Ala	Val	Ser	Thr	Val	Thr	Ser	Val	Val	Pro	Ser	Thr
Ser	Ser	Ala	Leu	Thr	Gly	His	Ser	Ser	Ser	Pro	Ile	Gln	Ala	Gly	Leu
Ala	Val	Pro	Val	Thr	Arg	Pro	Pro	Ser	Val	Ala	Pro	Val	Thr	Pro	Thr
Ser	Gly	Ala	Ile	Ser	Asp	Thr	Glu	Ala	Thr	Thr	Met	Tyr	Tyr	Phe	Ser
305															320
Leu	Gly	Ser	Phe	Ala	Glu	Asn	Lys	Glu	Met	Ser	Val	Asn	Gly	Lys	Ala
Asn	Leu	Ser	Pro	Ala	Gly	Asp	Lys	Ala	Asn	Val	Glu	Glu	Pro	Met	Val
Tyr	Ala	Thr	Lys	Gln	Glu	Ala	Lys	Ala	Ala	Phe	Lys	Ser	Leu	Leu	Glu
Ser	Val	Asn	Val	His	Ser	Asp	Trp	Thr	Trp	Glu	Gln	Thr	Leu	Lys	Glu
Ile	Val	His	Asp	Lys	Arg	Tyr	Gly	Ala	Leu	Arg	Thr	Leu	Gly	Glu	Arg
385															400
Lys	Gln	Ala	Phe	Asn	Glu	Tyr	Leu	Gly	Gln	Arg	Lys	Lys	Val	Glu	Ala
		</													

565 570 575
 Glu Glu His Val Ala Ala Gly Ile Leu Thr Ala Lys Thr Tyr Trp Leu
 580 585 590
 Asp Tyr Cys Ile Glu Leu Lys Asp Leu Pro Gln Tyr Gln Ala Val Ala
 595 600 605
 Ser Asn Thr Ser Gly Ser Thr Pro Lys Asp Leu Phe Glu Asp Val Thr
 610 615 620
 Glu Glu Leu Glu Lys Gln Tyr His Glu Asp Lys Ser Tyr Val Lys Asp
 625 630 635 640
 Ala Met Lys Ser Arg Lys Ala Asn Phe Lys Ser Ala Ile Ser Glu Asp
 645 650 655
 Leu Ser Thr Gln Gln Ile Ser Asp Ile Asn Leu Lys Leu Ile Tyr Asp
 660 665 670
 Asp Leu Val Gly Arg Val Lys Glu Lys Glu Glu Lys Glu Ala Arg Lys
 675 680 685
 Leu Gln Arg Leu Ala Glu Glu Phe Thr Asn Leu Leu His Thr Phe Lys
 690 695 700
 Glu Ile Thr Val Ala Ser Asn Trp Glu Asp Ser Lys Gln Leu Val Glu
 705 710 715 720
 Glu Ser Gln Glu Tyr Arg Ser Ile Gly Asp Glu Ser Val Ser Gln Gly
 725 730 735
 Leu Phe Glu Glu Tyr Ile Thr Ser Leu Gln Glu Lys Ala Lys Glu Lys
 740 745 750
 Glu Arg Lys Arg Asp Glu Glu Lys Val Arg Lys Glu Lys Glu Arg Asp
 755 760 765
 Glu Lys Glu Lys Arg Lys Asp Lys Asp Lys Glu Arg Arg Glu Lys Glu
 770 775 780
 Arg Glu Arg Glu Lys Glu Lys Gly Lys Glu Arg Ser Lys Arg Glu Glu
 785 790 795 800
 Ser Asp Gly Glu Thr Ala Met Asp Val Ser Glu Gly His Lys Asp Glu
 805 810 815
 Lys Arg Lys Gly Lys Asp Arg Asp Arg Lys His Arg Arg Arg His His
 820 825 830
 Asn Asn Ser Asp Glu Asp Val Ser Ser Asp Arg Asp Asp Arg Asp Glu
 835 840 845
 Ser Lys Lys Ser Ser Arg Lys His Gly Asn Asp Arg Lys Lys Ser Arg
 850 855 860
 Lys His Ala Asn Ser Pro Glu Ser Glu Ser Glu Asn Arg His Lys Arg
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 Gln Lys Lys Glu Ser Ser Arg Arg Ser Gly Asn Asp Glu Leu Glu Asp
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 Gly Glu Val Gly Glu
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 <211> 358
 <212> PRT
 <213> Arabidopsis thaliana

<400> 109
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 35 40 45

Trp Glu Asn Asp Pro His Tyr Phe Lys Arg Val Lys Ile Ser Ala Leu
 50 55 60
 Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu
 65 70 75 80
 Ile Met Gly Leu Met Gln Gly Lys Thr Asp Gly Asp Thr Ile Ile Val
 85 90 95
 Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn
 100 105 110
 Ala Gln Asp Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Asn
 115 120 125
 Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His
 130 135 140
 Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Arg
 145 150 155 160
 Leu Asn Gln Gln His Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro
 165 170 175
 Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr
 180 185 190
 Tyr Ser Lys Gly Tyr Lys Pro Pro Asp Glu Pro Val Ser Glu Tyr Gln
 195 200 205
 Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln
 210 215 220
 Tyr Tyr Ser Leu Asp Val Thr Tyr Phe Lys Ser Ser Leu Asp Ser His
 225 230 235 240
 Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser
 245 250 255
 Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp
 260 265 270
 Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser His Leu Val Gln Ser Arg
 275 280 285
 Phe Gly Gly Val Val Pro Ser Ser Leu His Lys Lys Lys Glu Asp Glu
 290 295 300
 Ser Gln Leu Thr Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu
 305 310 315 320
 Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Glu Leu Phe Asn
 325 330 335
 Ser Met Arg Gln Ser Asn Asn Lys Ser Pro Thr Asp Ser Ser Asp Pro
 340 345 350
 Asp Pro Met Ile Thr Tyr
 355

<210> 110

<211> 98

<212> PRT

<213> Arabidopsis thaliana

<400> 110

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 20 25 30
 Gly Tyr Ala Lys Lys Ile Asp Cys Gly Ser Ala Cys Val Ala Arg Cys
 35 40 45
 Arg Leu Ser Arg Arg Pro Arg Leu Cys His Arg Ala Cys Gly Thr Cys
 50 55 60
 Cys Tyr Arg Cys Asn Cys Val Pro Pro Gly Thr Tyr Gly Asn Tyr Asp


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			20					25					30		
Asn	Lys	Asn	Lys	Lys	Lys	Arg	Ser	His	Glu	Asp	Thr	Glu	Ile	Glu	Pro
		35					40					45			
Glu	Gln	Lys	Met	Ser	Leu	Asp	Gly	Asp	Ser	Arg	Glu	Glu	Lys	Ile	Lys
	50					55					60				
Lys	Lys	Arg	Lys	Asn	Lys	Asn	Gln	Glu	Glu	Glu	Pro	Glu	Leu	Val	Thr
65					70					75					80
Glu	Lys	Thr	Lys	Val	Gln	Glu	Glu	Glu	Lys	Gly	Asn	Val	Glu	Glu	Gly
				85					90					95	
Arg	Ala	Thr	Val	Ser	Ile	Ala	Ile	Ala	Gly	Ser	Ile	Ile	His	Asn	Thr
			100					105					110		
Gln	Ser	Leu	Glu	Leu	Ala	Thr	Arg	Val	Ile	Ser	Leu	Ser	Leu	Tyr	Leu
		115					120					125			
Ser	Leu	Arg	Phe	Ser	Val	Phe	Pro	Phe	Pro	Asp	Asn	Leu	Lys	Ser	Pro
	130					135					140				
Ser	Ser	Ile	Ser	Asn	Ile	Ser	Gln	Leu	Ala	Gly	Gln	Ile	Ala	Arg	Ala
145					150					155					160
Ala	Thr	Ile	Phe	Arg	Ile	Asp	Glu	Ile	Val	Val	Phe	Asp	Asn	Lys	Ser
				165					170					175	
Ser	Ser	Glu	Ile	Glu	Ser	Ala	Ala	Thr	Asn	Ala	Ser	Asp	Ser	Asn	Glu
			180					185					190		
Ser	Gly	Ala	Ser	Phe	Leu	Val	Arg	Ile	Leu	Lys	Tyr	Leu	Glu	Thr	Pro
	195						200					205			
Gln	Tyr	Leu	Arg	Lys	Ser	Leu	Phe	Pro	Lys	Gln	Asn	Asp	Leu	Arg	Tyr
	210					215					220				
Val	Gly	Met	Leu	Pro	Gly	Met	Leu	Pro	Pro	Leu	Asp	Ala	Pro	His	His
225					230					235					240
Leu	Arg	Lys	His	Glu	Trp	Glu	Gln	Tyr	Arg	Glu	Xaa	Xaa	Ile	Val	Pro
				245					250					255	
Pro	Ser	Lys	Pro	Arg	Glu	Glu	Ala	Gly	Met	Tyr	Trp	Gly	Tyr	Lys	Val
			260					265					270		
Arg	Tyr	Ala	Ser	Gln	Leu	Ser	Ser	Val	Phe	Lys	Glu	Cys	Pro	Phe	Glu
		275					280					285			
Gly	Gly	Tyr	Asp	Tyr	Leu	Ile	Gly	Thr	Ser	Glu	His	Gly	Leu	Val	Ile
	290					295					300				
Ser	Ser	Ser	Glu	Leu	Lys	Ile	Pro	Thr	Phe	Arg	His	Leu	Leu	Ile	Ala

305					310					315					320
Phe	Gly	Gly	Leu	Ala	Gly	Leu	Glu	Glu	Ser	Ile	Glu	Asp	Asp	Asn	Gln
				325					330					335	
Tyr	Lys	Gly	Lys	Asn	Val	Arg	Asp	Val	Phe	Asn	Val	Tyr	Leu	Asn	Thr
				340					345					350	
Cys	Pro	His	Gln	Gly	Ser	Arg	Thr	Ile	Arg	Ala	Glu	Glu	Ala	Met	Phe
				355					360					365	
Ile	Ser	Leu	Gln	Tyr	Phe	Gln	Glu	Pro	Ile	Ser	Arg	Ala	Val	Arg	Arg
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Leu															
385															

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<211> 465
<212> PRT
<213> Arabidopsis thaliana
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Val	Ala	Val	Leu	Arg	Phe	Leu	Leu	Cys	Phe	Val	Ala	Thr	Ile	Pro	Ile
			20					25					30		
Ser	Phe	Leu	Trp	Arg	Phe	Ile	Pro	Ser	Arg	Leu	Gly	Lys	His	Ile	Tyr
		35					40					45			
Ser	Ala	Ala	Ser	Gly	Ala	Phe	Leu	Ser	Tyr	Leu	Ser	Phe	Gly	Phe	Ser
	50					55					60				
Ser	Asn	Leu	His	Phe	Leu	Val	Pro	Met	Thr	Ile	Gly	Tyr	Ala	Ser	Met
65				70						75					80
Ala	Ile	Tyr	Arg	Pro	Leu	Ser	Gly	Phe	Ile	Thr	Phe	Phe	Leu	Gly	Phe
				85					90					95	
Ala	Tyr	Leu	Ile	Gly	Cys	His	Val	Phe	Tyr	Met	Ser	Gly	Asp	Ala	Trp
			100					105					110		
Lys	Glu	Gly	Gly	Ile	Asp	Ser	Thr	Gly	Ala	Leu	Met	Val	Leu	Thr	Leu
		115					120					125			
Lys	Val	Ile	Ser	Cys	Ser	Ile	Asn	Tyr	Asn	Asp	Gly	Met	Leu	Lys	Glu
	130					135					140				
Glu	Gly	Leu	Arg	Glu	Ala	Gln	Lys	Lys	Asn	Arg	Leu	Ile	Gln	Met	Pro
145				150						155					160
Ser	Leu	Ile	Glu	Tyr	Phe	Gly	Tyr	Cys	Leu	Cys	Cys	Gly	Ser	His	Phe
				165					170					175	
Ala	Gly	Pro	Val	Phe	Glu	Met	Lys	Asp	Tyr	Leu	Glu	Trp	Thr	Glu	Glu
			180					185					190		
Lys	Gly	Ile	Trp	Ala	Val	Ser	Glu	Lys	Gly	Lys	Arg	Pro	Ser	Pro	Tyr
		195					200					205			
Gly	Ala	Met	Ile	Arg	Ala	Val	Phe	Gln	Ala	Ala	Ile	Cys	Met	Ala	Leu
	210					215					220				
Tyr	Leu	Tyr	Leu	Val	Pro	Gln	Phe	Pro	Leu	Thr	Arg	Phe	Thr	Glu	Pro
225				230						235					240
Val	Tyr	Gln	Glu	Trp	Gly	Phe	Leu	Lys	Arg	Phe	Gly	Tyr	Gln	Tyr	Met
				245					250					255	
Ala	Gly	Phe	Thr	Ala	Arg	Trp	Lys	Tyr	Tyr	Phe	Ile	Trp	Ser	Ile	Ser
			260					265					270		
Glu	Ala	Ser	Ile	Ile	Ile	Ser	Gly	Leu	Gly	Phe	Ser	Gly	Trp	Thr	Asp
		275					280					285			
Glu	Thr	Gln	Thr	Lys	Ala	Lys	Trp	Asp	Arg	Ala	Lys	Asn	Val	Asp	Ile
	290					295					300				

Leu Gly Val Glu Leu Ala Lys Ser Ala Val Gln Ile Pro Leu Phe Trp
 305 310 315 320
 Asn Ile Gln Val Ser Thr Trp Leu Arg His Tyr Val Tyr Glu Arg Ile
 325 330 335
 Val Lys Pro Gly Lys Lys Ala Gly Phe Phe Gln Leu Leu Ala Thr Gln
 340 345 350
 Thr Val Ser Ala Val Trp His Gly Leu Tyr Pro Gly Tyr Ile Ile Phe
 355 360 365
 Phe Val Gln Ser Ala Leu Met Ile Asp Gly Ser Lys Ala Ile Tyr Arg
 370 375 380
 Trp Gln Gln Ala Ile Pro Pro Lys Met Ala Met Leu Arg Asn Val Leu
 385 390 395 400
 Val Leu Ile Asn Phe Leu Tyr Thr Val Val Val Leu Asn Tyr Ser Ser
 405 410 415
 Val Gly Phe Met Val Leu Ser Leu His Glu Thr Leu Val Ala Phe Lys
 420 425 430
 Ser Val Tyr Tyr Ile Gly Thr Val Ile Pro Ile Ala Val Leu Leu Leu
 435 440 445
 Ser Tyr Leu Val Pro Val Lys Pro Val Arg Pro Lys Thr Arg Lys Glu
 450 455 460
 Glu
 465

<210> 113
 <211> 313
 <212> PRT
 <213> Arabidopsis thaliana

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 Leu Glu Lys Val Gly Glu Gly Thr Tyr Gly Lys Val Tyr Arg Ala Arg
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 Glu Lys Ala Thr Gly Lys Ile Val Ala Leu Lys Lys Thr Arg Leu His
 35 40 45
 Glu Asp Glu Glu Gly Val Pro Ser Thr Thr Leu Arg Glu Ile Ser Ile
 50 55 60
 Leu Arg Met Leu Ala Arg Asp Pro His Val Val Arg Leu Met Asp Val
 65 70 75 80
 Lys Gln Gly Leu Ser Lys Glu Gly Lys Thr Val Leu Tyr Leu Val Phe
 85 90 95
 Glu Tyr Met Asp Thr Asp Val Lys Lys Phe Ile Arg Ser Phe Arg Ser
 100 105 110
 Thr Gly Lys Asn Ile Pro Thr Gln Thr Ile Lys Ser Leu Met Tyr Gln
 115 120 125
 Leu Cys Lys Gly Met Ala Phe Cys His Gly His Gly Ile Leu His Arg
 130 135 140
 Asp Leu Lys Pro His Asn Leu Leu Met Asp Pro Lys Thr Met Arg Leu
 145 150 155 160
 Lys Ile Ala Asp Leu Gly Leu Ala Arg Ala Phe Thr Leu Pro Met Lys
 165 170 175
 Lys Tyr Thr His Glu Ile Leu Thr Leu Trp Tyr Arg Ala Pro Glu Val
 180 185 190
 Leu Leu Gly Ala Thr His Tyr Ser Thr Ala Val Asp Met Trp Ser Val
 195 200 205
 Gly Cys Ile Phe Ala Glu Leu Val Thr Asn Gln Ala Ile Phe Gln Gly

210	215	220
Asp Ser Glu Leu Gln Gln Leu Leu His Ile Phe Lys Leu Phe Gly Thr		
225	230	235
Pro Asn Glu Glu Met Trp Pro Gly Val Ser Thr Leu Lys Asn Trp His		240
	245	250
Glu Tyr Pro Gln Trp Lys Pro Ser Thr Leu Ser Ser Ala Val Pro Asn		255
	260	265
Leu Asp Glu Ala Gly Val Asp Leu Leu Ser Lys Met Leu Gln Tyr Glu		270
	275	280
Pro Ala Lys Arg Ile Ser Ala Lys Met Ala Met Glu His Pro Tyr Phe		285
	290	295
Asp Asp Leu Pro Glu Lys Ser Ser Leu		300
305	310	

<210> 114
 <211> 292
 <212> PRT
 <213> Arabidopsis thaliana

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 His Pro Ser Val Ser Val Glu Lys Thr Pro Val Arg Arg Lys Leu Ile
 20 25 30
 Val Asp Asp Asp Ser Glu Ile Gly Ser Glu Lys Lys Gly Gln Ser Arg
 35 40 45
 Thr Ser Gly Gly Gly Leu Arg Gln Phe Ser Val Met Val Cys Gln Lys
 50 55 60
 Leu Glu Ala Lys Lys Ile Thr Thr Tyr Lys Glu Val Ala Asp Glu Ile
 65 70 75 80
 Ile Ser Asp Phe Ala Thr Ile Lys Gln Asn Ala Glu Lys Pro Leu Asn
 85 90 95
 Glu Asn Glu Tyr Asn Glu Lys Asn Ile Arg Arg Arg Val Tyr Asp Ala
 100 105 110
 Leu Asn Val Phe Met Ala Leu Asp Ile Ile Ala Arg Asp Lys Lys Glu
 115 120 125
 Ile Arg Trp Lys Gly Leu Pro Ile Thr Cys Lys Lys Asp Val Glu Glu
 130 135 140
 Val Lys Met Asp Arg Asn Lys Val Met Ser Ser Val Gln Lys Lys Ala
 145 150 155 160
 Ala Phe Leu Lys Glu Leu Arg Glu Lys Val Ser Ser Leu Glu Ser Leu
 165 170 175
 Met Ser Arg Asn Gln Glu Met Val Val Lys Thr Gln Gly Pro Ala Glu
 180 185 190
 Gly Phe Thr Leu Pro Phe Ile Leu Leu Glu Thr Asn Pro His Ala Val
 195 200 205
 Val Glu Ile Glu Ile Ser Glu Asp Met Gln Leu Val His Leu Asp Phe
 210 215 220
 Asn Ser Thr Pro Phe Ser Val His Asp Asp Ala Tyr Ile Leu Lys Leu
 225 230 235 240
 Met Gln Glu Gln Lys Gln Glu Gln Asn Arg Val Ser Ser Ser Ser Ser
 245 250 255
 Thr His His Gln Ser Gln His Ser Ser Ala His Ser Ser Ser Ser
 260 265 270
 Cys Ile Ala Ser Gly Thr Ser Gly Pro Val Cys Trp Asn Ser Gly Ser
 275 280 285

Ile Asp Thr Arg
290

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<211> 165
<212> PRT
<213> Arabidopsis thaliana

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Met Asn Arg Glu Lys Leu Met Lys Met Ala Asn Thr Val Arg Thr Gly
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Gly Lys Gly Thr Val Arg Arg Lys Lys Lys Ala Val His Lys Thr Thr
20 25 30
Thr Thr Asp Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Val Gly Val
35 40 45
Asn Ser Ile Pro Ala Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val
50 55 60
Val Ile Gln Phe Ile Asn Pro Lys Val Gln Ala Ser Ile Ala Ala Asn
65 70 75 80
Thr Trp Val Val Ser Gly Thr Pro Gln Thr Lys Lys Leu Gln Asp Ile
85 90 95
Leu Pro Gln Ile Ile Ser Gln Leu Gly Pro Asp Asn Leu Asp Asn Leu
100 105 110
Lys Lys Leu Ala Glu Gln Phe Gln Lys Gln Ala Pro Gly Ala Gly Asp
115 120 125
Val Pro Ala Thr Ile Gln Glu Glu Asp Asp Asp Asp Val Pro Asp
130 135 140
Leu Val Val Gly Glu Thr Phe Glu Thr Pro Ala Thr Glu Glu Ala Pro
145 150 155 160
Lys Ala Ala Ala Ser
165

<210> 116
<211> 432
<212> PRT
<213> Arabidopsis thaliana

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Met Ala Thr Val Ser Ser Ser Trp Pro Asn Pro Asn Pro Asn Pro
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Asp Ser Thr Ser Ala Ser Asp Ser Asp Thr Phe Pro Ser His Arg
20 25 30
Asp Arg Val Asp Glu Pro Asp Ser Leu Asp Ser Phe Ser Ser Met Ser
35 40 45
Leu Asn Ser Asp Glu Pro Asn Gln Thr Ser Asn Gln Ser Pro Leu Ser
50 55 60
Pro Pro Thr Pro Asn Leu Pro Val Met Pro Pro Pro Ser Val Leu His
65 70 75 80
Leu Ser Phe Asn Gln Asp His Ala Cys Phe Ala Val Gly Thr Asp Arg
85 90 95
Gly Phe Arg Ile Leu Asn Cys Asp Pro Phe Arg Glu Ile Phe Arg Arg
100 105 110
Asp Phe Asp Arg Gly Gly Gly Val Ala Val Val Glu Met Leu Phe Arg
115 120 125
Cys Asn Ile Leu Ala Leu Val Gly Gly Gly Pro Asp Pro Gln Tyr Pro

130	135	140													
Pro Asn Lys Val Met Ile Trp Asp Asp His Gln Gly Arg Cys Ile Gly															
145	150	155													160
Glu Leu Ser Phe Arg Ser Asp Val Arg Ser Val Arg Leu Arg Arg Asp															
	165	170													175
Arg Ile Ile Val Val Leu Glu Gln Lys Ile Phe Val Tyr Asn Phe Ser															
	180	185													190
Asp Leu Lys Leu Met His Gln Ile Glu Thr Ile Ala Asn Pro Lys Gly															
	195	200													205
Leu Cys Ala Val Ser Gln Gly Val Gly Ser Met Val Leu Val Cys Pro															
	210	215													220
Gly Leu Gln Lys Gly Gln Val Arg Ile Glu His Tyr Ala Ser Lys Arg															
225	230	235													240
Thr Lys Phe Val Met Ala His Asp Ser Arg Ile Ala Cys Phe Ala Leu															
	245	250													255
Thr Gln Asp Gly His Leu Leu Ala Thr Ala Ser Ser Lys Gly Thr Leu															
	260	265													270
Val Arg Ile Phe Asn Thr Val Asp Gly Thr Leu Arg Gln Glu Ser Gly															
	275	280													285
Thr Ser Glu Asp Glu Ile Gly Lys Glu Gly Ala Asp Arg Ala Glu Ile															
	290	295													300
Tyr Ser Leu Ala Phe Ser Ser Asn Ala Gln Trp Leu Ala Val Ser Ser															
305	310	315													320
Asp Lys Gly Thr Val His Val Phe Gly Leu Lys Val Asn Ser Gly Ser															
	325	330													335
Gln Val Lys Asp Ser Ser Arg Ile Ala Pro Asp Ala Thr Pro Ser Ser															
	340	345													350
Pro Ser Ser Ser Leu Ser Leu Phe Lys Val Leu Pro Arg Tyr Phe Ser															
	355	360													365
Ser Glu Trp Ser Val Ala Gln Phe Arg Leu Val Glu Gly Thr Gln Tyr															
	370	375													380
Ile Ala Ala Phe Gly His Gln Lys Asn Thr Val Val Ile Leu Gly Met															
385	390	395													400
Asp Gly Ser Phe Tyr Arg Cys Gln Phe Asp Pro Val Asn Gly Gly Glu															
	405	410													415
Met Ser Gln Leu Glu Tyr His Asn Cys Leu Lys Pro Pro Ser Val Phe															
	420	425													430

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 <212> PRT
 <213> Arabidopsis thaliana

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 Lys Leu Leu Thr Glu Glu Asp Ile Ser Gln Leu Thr Arg Glu Asp Cys
 20 25 30
 Arg Lys Phe Leu Lys Glu Lys Gly Phe Phe Phe Phe Leu Ser Pro Phe
 35 40 45
 Phe Ser Gly Leu Ile Val Phe Asp Glu Trp Arg Leu Thr Arg Val Glu
 50 55 60
 Thr Gly Met Arg Arg Pro Ser Trp Asn Lys Ser Gln Ala Ile Gln Gln
 65 70 75 80
 Val Leu Ser Leu Lys Ala Leu Tyr Glu Pro Gly Asp Asp Ser Gly Ala
 85 90 95

Gly Ile Leu Arg Lys Ile Leu Val Ser Gln Pro Pro Asn Pro Pro Arg
 100 105 110
 Val Thr Thr Thr Leu Ile Glu Pro Arg Asn Glu Leu Glu Ala Cys Gly
 115 120 125
 Arg Ile Pro Leu Gln Glu Asp Asp Gly Ala Cys His Arg Arg Asp Ser
 130 135 140
 Pro Arg Ser Ala Glu Phe Ser Gly Ser Ser Gly Gln Phe Val Ala Asp
 145 150 155 160
 Lys Asp Ser His Lys Thr Val Ser Val Ser Pro Arg Ser Pro Ala Glu
 165 170 175
 Thr Asn Ala Val Val Gly Gln Met Thr Ile Phe Tyr Ser Gly Lys Val
 180 185 190
 Asn Val Tyr Asp Gly Val Pro Pro Glu Lys Ala Arg Ser Ile Met His
 195 200 205
 Phe Ala Ala Asn Pro Ile Asp Leu Pro Glu Asn Gly Ile Phe Ala Ser
 210 215 220
 Ser Arg Met Ile Ser Lys Pro Met Ser Lys Glu Lys Met Val Glu Leu
 225 230 235 240
 Pro Gln Tyr Gly Leu Glu Lys Ala Pro Ala Ser Arg Asp Ser Asp Val
 245 250 255
 Glu Gly Gln Ala Asn Arg Lys Val Ser Leu Gln Arg Tyr Leu Glu Lys
 260 265 270
 Arg Lys Asp Arg Phe Ser Lys Thr Lys Lys Ala Pro Gly Val Ala Ser
 275 280 285
 Ser Ser Leu Glu Met Phe Leu Asn Arg Gln Pro Arg Met Asn Ala Ala
 290 295 300
 Tyr Ser Gln Asn Leu Ser Gly Thr Gly His Cys Glu Ser Pro Glu Asn
 305 310 315 320
 Gln Thr Lys Ser Pro Asn Ile Ser Val Asp Leu Asn Ser Asp Leu Asn
 325 330 335
 Ser Glu Gly Ala Lys Arg Thr Gly Asp Gly Thr Thr Gly Gln Lys Ala
 340 345 350
 Gly Arg Thr Ile Ser Cys Ser Tyr Asn Met Thr Lys Thr Ser Arg Gly
 355 360 365
 Thr Arg Trp Val Lys Arg Ser Arg Glu Glu Val Ile Gln Ala Trp Tyr
 370 375 380
 Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Lys Asp Pro
 385 390 395 400
 Lys Glu Phe Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser
 405 410 415
 Trp Arg Leu Asp Ala Asp Asn Tyr Glu Thr Asp Glu Asp Leu Lys Lys
 420 425 430
 Ile Arg Glu Ser Arg Gly Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys
 435 440 445
 Pro Glu Lys Leu Pro Asn Tyr Glu Val Lys Val Lys Ser Phe Phe Glu
 450 455 460
 Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Val Ala Gly Thr
 465 470 475 480
 Gly Tyr Phe Asp Val Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Leu
 485 490 495
 Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg
 500 505 510
 Phe Thr Val Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe Val
 515 520 525
 Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro
 530 535 540
 Ala Arg Lys Glu Tyr Val Asp Asn Phe Met Ile Asn Ala Ser Ala

545

550

555

<210> 118
 <211> 86
 <212> PRT
 <213> Arabidopsis thaliana

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 Thr Ala Phe Val Gln Asn Leu Leu Gln Gln Met Gln Thr Arg Phe Gln
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 Thr Met Ser Asp Ser Ile Ile Thr Lys Ile Asp Asp Met Gly Gly Arg
 35 40 45
 Ile Asn Glu Leu Glu Gln Ser Ile Asn Asp Leu Arg Ala Glu Met Gly
 50 55 60
 Val Glu Gly Thr Pro Pro Ala Ser Lys Ser Gly Asp Glu Pro Lys
 65 70 75 80
 Thr Pro Ala Ser Ser
 85

<210> 119
 <211> 784
 <212> PRT
 <213> Arabidopsis thaliana

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 Met Glu Ile Tyr Thr Met Lys Thr Asn Phe Leu Val Leu Ala Leu Ser
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 20 25 30
 Gly Ser Gly Leu Ser Asn Leu Asp Leu Ile Glu Arg Asp Tyr Gln Asp
 35 40 45
 Ser Val Asn Ala Leu Gln Gly Lys Asp Asp Glu Asp Gln Ser Ala Lys
 50 55 60
 Ile Gln Ser Glu Asn Gln Asn Asn Thr Thr Val Thr Asp Lys Asn Thr
 65 70 75 80
 Ile Ser Leu Ser Leu Ser Asp Glu Ser Glu Val Gly Ser Val Ser Asp
 85 90 95
 Glu Ser Val Gly Arg Ser Ser Leu Leu Asp Gln Ile Lys Leu Glu Phe
 100 105 110
 Glu Ala His His Asn Ser Ile Asn Gln Ala Gly Ser Asp Gly Val Lys
 115 120 125
 Ala Glu Ser Lys Asp Asp Asp Glu Glu Leu Ser Ala His Arg Gln Lys
 130 135 140
 Met Leu Glu Glu Ile Glu His Glu Phe Glu Ala Ala Ser Asp Ser Leu
 145 150 155 160
 Lys Gln Leu Lys Thr Asp Asp Val Asn Glu Gly Asn Asp Glu Glu His
 165 170 175
 Ser Ala Lys Arg Gln Ser Leu Leu Glu Glu Ile Glu Arg Glu Phe Glu
 180 185 190
 Ala Ala Thr Lys Glu Leu Glu Gln Leu Lys Val Asn Asp Phe Thr Gly
 195 200 205
 Asp Lys Asp Asp Glu Glu His Ser Ala Lys Arg Lys Ser Met Leu Glu
 210 215 220

Ala Ile Glu Arg Glu Phe Glu Ala Ala Met Glu Gly Ile Glu Ala Leu
 225 230 235 240
 Lys Val Ser Asp Ser Thr Gly Ser Gly Asp Asp Glu Glu Gln Ser Ala
 245 250 255
 Lys Arg Leu Ser Met Leu Glu Glu Ile Glu Arg Glu Phe Glu Ala Ala
 260 265 270
 Ser Lys Gly Leu Glu Gln Leu Arg Ala Ser Asp Ser Thr Ala Asp Asn
 275 280 285
 Asn Glu Glu Glu His Ala Ala Lys Gly Gln Ser Leu Leu Glu Glu Ile
 290 295 300
 Glu Arg Glu Phe Glu Ala Ala Thr Glu Ser Leu Lys Gln Leu Gln Val
 305 310 315 320
 Asp Asp Ser Thr Glu Asp Lys Glu His Cys Lys Ala Leu Phe Phe Leu
 325 330 335
 Leu Ser Ala Ile Leu Ser Leu Trp Leu Ser Glu Ser Gly Phe Glu Cys
 340 345 350
 Ile Val Val Thr Ala Ala Lys Arg Gln Ser Leu Leu Glu Glu Ile Glu
 355 360 365
 Arg Glu Phe Glu Ala Ala Thr Lys Asp Leu Lys Gln Leu Asn Asp Phe
 370 375 380
 Thr Glu Gly Ser Ala Asp Asp Glu Gln Ser Ala Lys Arg Asn Lys Met
 385 390 395 400
 Leu Glu Asp Ile Glu Arg Glu Phe Glu Ala Ala Thr Ile Gly Leu Glu
 405 410 415
 Gln Leu Lys Ala Asn Asp Phe Ser Glu Gly Asn Asn Asn Glu Glu Gln
 420 425 430
 Ser Ala Lys Arg Lys Ser Met Leu Glu Glu Ile Glu Arg Glu Phe Glu
 435 440 445
 Ala Ala Ile Gly Gly Leu Lys Gln Ile Lys Val Asp Asp Ser Arg Asn
 450 455 460
 Leu Glu Glu Glu Ser Ala Lys Arg Lys Ile Ile Leu Glu Glu Met Glu
 465 470 475 480
 Arg Glu Phe Glu Glu Ala His Ser Gly Ile Asn Ala Lys Ala Asp Lys
 485 490 495
 Glu Glu Ser Ala Lys Lys Gln Ser Gly Ser Ala Ile Pro Glu Val Leu
 500 505 510
 Gly Leu Gly Gln Ser Gly Gly Cys Ser Cys Ser Lys Gln Asp Glu Asp
 515 520 525
 Ser Ser Ile Val Ile Pro Thr Lys Tyr Ser Ile Glu Asp Ile Leu Ser
 530 535 540
 Glu Glu Ser Ala Val Gln Gly Thr Glu Thr Ser Ser Leu Thr Ala Ser
 545 550 555 560
 Leu Thr Gln Leu Val Glu Asn His Arg Lys Glu Lys Glu Ser Leu Leu
 565 570 575
 Gly His Arg Val Leu Thr Ser Pro Ser Ile Ala Ser Ser Thr Ser Glu
 580 585 590
 Ser Ser Ala Thr Ser Glu Thr Val Glu Thr Leu Arg Ala Lys Leu Asn
 595 600 605
 Glu Leu Arg Gly Leu Thr Ala Arg Glu Leu Val Thr Arg Lys Asp Phe
 610 615 620
 Gly Gln Ile Leu Ile Thr Ala Ala Ser Phe Glu Leu Ser Ser Ala
 625 630 635 640
 Pro Ile Ser Tyr Ile Ser Arg Leu Ala Lys Tyr Arg Asn Val Ile Lys
 645 650 655
 Glu Gly Leu Glu Ala Ser Glu Arg Val His Ile Ala Gln Val Arg Ala
 660 665 670
 Lys Met Leu Lys Glu Val Ala Thr Glu Lys Gln Thr Ala Val Asp Thr

		675					680					685						
His	Phe	Ala	Thr	Ala	Lys	Lys	Leu	Ala	Gln	Glu	Gly	Asp	Ala	Leu	Phe			
	690					695					700							
Val	Lys	Ile	Phe	Ala	Ile	Lys	Lys	Leu	Leu	Ala	Lys	Leu	Glu	Ala	Glu			
705					710					715					720			
Lys	Glu	Ser	Val	Asp	Gly	Lys	Phe	Lys	Glu	Thr	Val	Lys	Glu	Leu	Ser			
				725					730					735				
His	Leu	Leu	Ala	Asp	Ala	Ser	Glu	Ala	Tyr	Glu	Glu	Tyr	His	Gly	Ala			
			740					745					750					
Val	Arg	Lys	Ala	Lys	Asp	Glu	Gln	Ala	Ala	Glu	Glu	Phe	Ala	Lys	Glu			
		755					760					765						
Ala	Thr	Gln	Ser	Ala	Glu	Ile	Ile	Trp	Val	Lys	Phe	Leu	Ser	Ser	Leu			
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<210> 120
<211> 724
<212> PRT
<213> Arabidopsis thaliana
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			20					25					30		
Asn	Ala	Pro	Ile	Tyr	Tyr	Pro	Asn	Arg	Ile	Leu	Lys	Gly	Leu	Glu	Pro
		35					40					45			
Trp	Glu	Gly	Thr	Ser	Leu	Thr	Arg	Asn	Pro	Phe	Ala	Trp	Met	Arg	Glu
	50					55					60				
Ala	Leu	Thr	Ser	Ser	Glu	Gln	Asp	Val	Val	Asn	Leu	Ser	Gly	Val	Asp
65					70					75					80
Thr	Ala	Val	His	Phe	Val	Phe	Leu	Ser	Thr	Val	Leu	Gly	Ile	Phe	Ala
				85					90					95	
Cys	Ser	Ser	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Leu	Pro	Leu	Ala	Ala	Thr
			100					105					110		
Asp	Asn	Asn	Ile	Lys	Asn	Thr	Lys	Asn	Ala	Thr	Asp	Thr	Thr	Ser	Lys
		115					120					125			
Gly	Thr	Phe	Ser	Gln	Leu	Asp	Asn	Leu	Ser	Met	Ala	Asn	Ile	Thr	Lys
	130					135					140				
Lys	Ser	Ser	Arg	Leu	Trp	Ala	Phe	Leu	Gly	Ala	Val	Tyr	Trp	Ile	Ser
145					150					155					160
Leu	Val	Thr	Tyr	Phe	Phe	Leu	Trp	Lys	Ala	Tyr	Lys	His	Val	Ser	Ser
				165					170					175	
Leu	Arg	Ala	Gln	Ala	Leu	Met	Ser	Ala	Asp	Val	Lys	Pro	Glu	Gln	Phe
			180					185					190		
Ala	Ile	Leu	Val	Arg	Asp	Met	Pro	Ala	Pro	Pro	Asp	Gly	Gln	Thr	Gln
		195					200					205			
Lys	Glu	Phe	Ile	Asp	Ser	Tyr	Phe	Arg	Glu	Ile	Tyr	Pro	Glu	Thr	Phe
	210					215					220				
Tyr	Arg	Ser	Leu	Val	Ala	Thr	Glu	Asn	Ser	Lys	Val	Asn	Lys	Ile	Trp
225					230					235					240
Glu	Lys	Leu	Glu	Gly	Tyr	Lys	Lys	Lys	Leu	Ala	Arg	Ala	Glu	Ala	Ile
				245					250					255	
Leu	Ala	Ala	Thr	Asn	Asn	Arg	Pro	Thr	Asn	Lys	Thr	Gly	Phe	Cys	Gly
			260					265					270		
Leu	Val	Gly	Lys	Gln	Val	Asp	Ser	Ile	Glu	Tyr	Tyr	Thr	Glu	Leu	Ile
		275					280						285		

Asn	Glu	Ser	Val	Ala	Lys	Leu	Glu	Thr	Glu	Gln	Lys	Ala	Val	Leu	Ala
290						295					300				
Glu	Lys	Gln	Gln	Thr	Ala	Ala	Val	Val	Phe	Phe	Thr	Thr	Arg	Val	Ala
305					310					315					320
Ala	Ala	Ser	Ala	Ala	Gln	Ser	Leu	His	Cys	Gln	Met	Val	Asp	Lys	Trp
				325					330					335	
Thr	Val	Thr	Glu	Ala	Pro	Glu	Pro	Arg	Gln	Leu	Leu	Trp	Gln	Asn	Leu
			340					345					350		
Asn	Ile	Lys	Leu	Phe	Ser	Arg	Ile	Ile	Arg	Gln	Tyr	Phe	Ile	Tyr	Phe
		355					360					365			
Phe	Val	Ala	Val	Thr	Ile	Leu	Phe	Tyr	Met	Ile	Pro	Ile	Ala	Phe	Val
						375					380				
Ser	Ala	Ile	Thr	Thr	Leu	Lys	Asn	Leu	Gln	Arg	Ile	Ile	Pro	Phe	Ile
385					390					395					400
Lys	Pro	Val	Val	Glu	Ile	Thr	Ala	Ile	Arg	Thr	Val	Leu	Glu	Ser	Phe
				405					410					415	
Leu	Pro	Gln	Ile	Ala	Leu	Ile	Val	Phe	Leu	Ala	Met	Leu	Pro	Lys	Leu
			420					425					430		
Leu	Leu	Phe	Leu	Ser	Lys	Ala	Glu	Gly	Ile	Pro	Ser	Gln	Ser	His	Ala
		435					440					445			
Ile	Arg	Ala	Ala	Ser	Gly	Lys	Tyr	Phe	Tyr	Phe	Ser	Val	Phe	Asn	Val
		450				455					460				
Phe	Ile	Gly	Val	Thr	Leu	Ala	Gly	Thr	Leu	Phe	Asn	Thr	Val	Lys	Asp
465					470					475					480
Ile	Ala	Lys	Asn	Pro	Lys	Leu	Asp	Met	Ile	Ile	Asn	Leu	Leu	Ala	Thr
				485					490					495	
Ser	Leu	Pro	Lys	Ser	Ala	Thr	Phe	Phe	Leu	Thr	Tyr	Val	Ala	Leu	Lys
			500					505					510		
Phe	Phe	Ile	Gly	Tyr	Gly	Leu	Glu	Leu	Ser	Arg	Ile	Ile	Pro	Leu	Ile
		515					520					525			
Ile	Phe	His	Leu	Lys	Lys	Lys	Tyr	Leu	Cys	Lys	Thr	Glu	Ala	Glu	Val
		530				535					540				
Lys	Glu	Ala	Trp	Tyr	Pro	Gly	Asp	Leu	Ser	Tyr	Ala	Thr	Arg	Val	Pro
545					550					555					560
Gly	Asp	Met	Leu	Ile	Leu	Thr	Ile	Thr	Phe	Cys	Tyr	Ser	Val	Ile	Ala
				565					570					575	
Pro	Leu	Ile	Leu	Ile	Phe	Gly	Ile	Thr	Tyr	Phe	Gly	Leu	Gly	Trp	Leu
			580					585					590		
Val	Leu	Arg	Asn	Gln	Ala	Leu	Lys	Val	Tyr	Val	Pro	Ser	Tyr	Glu	Ser
		595					600				605				
Tyr	Gly	Arg	Met	Trp	Pro	His	Ile	His	Gln	Arg	Ile	Leu	Ala	Ala	Leu
	610					615					620				
Phe	Leu	Phe	Gln	Val	Val	Met	Phe	Gly	Tyr	Leu	Gly	Ala	Lys	Thr	Phe
625					630					635					640
Phe	Tyr	Thr													

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 Pro Ser Ser Met Leu Arg Arg Tyr Ser Ile Pro Lys Asn Ser Leu Pro
 35 40 45
 Pro His Ser Ser Glu Leu Ala Ser Lys Val Gln Ser Leu Lys Asp Lys
 50 55 60
 Val Gln Leu Ala Lys Asp Asp Tyr Val Gly Leu Arg Gln Glu Ala Thr
 65 70 75 80
 Asp Leu Gln Glu Tyr Ser Asn Ala Lys Leu Glu Arg Val Thr Arg Tyr
 85 90 95
 Leu Gly Val Leu Ala Asp Lys Ser Arg Lys Leu Asp Gln Tyr Ala Leu
 100 105 110
 Glu Thr Glu Ala Arg Ile Ser Pro Leu Ile Asn Glu Lys Lys Arg Leu
 115 120 125
 Phe Asn Asp Leu Leu Thr Thr Lys Gly Ala His Leu Pro Phe Pro Thr
 130 135 140
 Ser Phe Ser Ile Leu Thr Ser Ile Asp Ile Asp His Thr Arg Pro Leu
 145 150 155 160
 Phe Glu Asp Glu Gly Pro Ser Ile Ile Glu Phe Pro Asp Asn Cys Thr
 165 170 175
 Ile Arg Val Asn Thr Ser Asp Asp Thr Leu Ser Asn Pro Lys Lys Glu
 180 185 190
 Phe Glu Phe Asp Arg Val Tyr Gly Pro Gln Val Gly Gln Ala Ser Leu
 195 200 205
 Phe Ser Asp Val Gln Pro Phe Val Gln Ser Ala Leu Asp Gly Ser Asn
 210 215 220
 Val Ser Ile Phe Ala Tyr Gly Gln Thr His Ala Gly Lys Thr Tyr Thr
 225 230 235 240
 Met Val Ala Pro Pro Phe Pro Phe Leu Ser Glu Ile Arg Tyr Arg Ser
 245 250 255
 Cys Leu Asp Leu Asn Met Ile Gly Lys Phe Met Asp Val His Ser Lys
 260 265 270
 Phe Met Asp Glu Gly Ser Asn Gln Asp Arg Gly Leu Tyr Ala Arg Cys
 275 280 285
 Phe Glu Glu Leu Met Asp Leu Ala Asn Ser Asp Ser Thr Ser Ala Ser
 290 295 300
 Gln Phe Ser Phe Ser Val Ser Val Phe Glu Leu Tyr Asn Glu Gln Val
 305 310 315 320
 Arg Asp Leu Leu Ser Gly Cys Gln Ser Asn Leu Pro Lys Ile Asn Met
 325 330 335
 Gly Leu Arg Glu Ser Val Ile Glu Leu Ser Gln Glu Lys Val Asp Asn
 340 345 350
 Pro Ser Glu Phe Met Arg Val Leu Asn Ser Ala Phe Gln Asn Arg Gly
 355 360 365
 Asn Asp Lys Ser Lys Ser Thr Val Thr His Leu Ile Val Ser Ile His
 370 375 380
 Ile Cys Tyr Ser Asn Thr Ile Thr Arg Glu Asn Val Ile Ser Lys Leu
 385 390 395 400

Ser Leu Val Asp Leu Ala Gly Ser Glu Gly Leu Thr Val Glu Asp Asp
 405 410 415
 Asn Gly Asp His Val Thr Asp Leu Leu His Val Thr Asn Ser Ile Ser
 420 425 430
 Ala Leu Gly Asp Val Leu Ser Ser Leu Thr Ser Lys Arg Asp Thr Ile
 435 440 445
 Pro Tyr Glu Asn Ser Phe Leu Thr Arg Ile Leu Ala Asp Ser Leu Gly
 450 455 460
 Gly Ser Ser Lys Thr Leu Met Ile Val Asn Ile Cys Pro Ser Ala Arg
 465 470 475 480
 Asn Leu Ser Glu Ile Met Ser Cys Leu Asn Tyr Ala Ala Arg Ala Arg
 485 490 495
 Asn Thr Val Pro Ser Leu Gly Asn Arg Asp Thr Ile Lys Lys Trp Arg
 500 505 510
 Asp Val Ala Asn Asp Ala Arg Lys Glu Val Leu Glu Lys Glu Arg Glu
 515 520 525
 Asn Gln Arg Leu Lys Gln Glu Val Thr Gly Leu Lys Gln Ala Leu Lys
 530 535 540
 Glu Ala Asn Asp Gln Cys Val Leu Leu Tyr Asn Glu Val Gln Arg Ala
 545 550 555 560
 Trp Arg Val Ser Phe Thr Leu Gln Ser Asp Leu Lys Ser Glu Asn Ala
 565 570 575
 Met Val Val Asp Lys His Lys Ile Glu Lys Glu Gln Asn Phe Gln Leu
 580 585 590
 Arg Asn Gln Ile Ala Gln Leu Leu Gln Leu Glu Gln Glu Lys Leu
 595 600 605
 Gln Ala Gln Gln Gln Asp Ser Thr Ile Gln Asn Leu Gln Ser Lys Val
 610 615 620
 Lys Asp Leu Glu Ser Gln Leu Ser Lys Ala Leu Lys Ser Asp Met Thr
 625 630 635 640
 Arg Ser Arg Asp Pro Leu Glu Pro Gln Pro Arg Ala Ala Glu Asn Thr
 645 650 655
 Leu Asp Ser Ser Ala Val Thr Lys Lys Leu Glu Glu Glu Leu Lys Lys
 660 665 670
 Arg Asp Ala Leu Ile Glu Arg Leu His Glu Glu Asn Glu Lys Leu Phe
 675 680 685
 Asp Arg Leu Thr Glu Lys Ser Val Ala Ser Ser Thr Gln Val Ser Ser
 690 695 700
 Pro Ser Ser Lys Ala Ser Pro Thr Val Gln Pro Ala Asp Val Asp Arg
 705 710 715 720
 Lys Asn Ser Ala Gly Thr Leu Pro Ser Ser Val Asp Lys Asn Glu Gly
 725 730 735
 Thr Ile Thr Leu Val Lys Ser Ser Ser Glu Leu Val Lys Thr Thr Pro
 740 745 750
 Ala Gly Glu Tyr Leu Thr Ala Ala Leu Asn Asp Phe Asp Pro Glu Gln
 755 760 765
 Tyr Glu Gly Leu Ala Ala Ile Ala Asp Gly Ala Asn Lys Leu Leu Met
 770 775 780
 Leu Val Leu Ala Ala Val Ile Lys Ala Gly Ala Ser Arg Glu His Glu
 785 790 795 800
 Ile Leu Ala Glu Ile Arg Asp Ser Val Phe Ser Phe Ile Arg Lys Met
 805 810 815
 Glu Pro Arg Arg Val Met Asp Thr Met Leu Val Ser Arg Val Arg Ile
 820 825 830
 Leu Tyr Ile Arg Ser Leu Leu Ala Arg Ser Pro Glu Leu Gln Ser Ile
 835 840 845
 Lys Val Ser Pro Val Glu Arg Phe Leu Glu Lys Pro Tyr Thr Gly Arg

850	855	860
Thr Arg Ser Ser Ser Gly	Ser Ser Ser Pro Gly	Arg Ser Pro Val Arg
865	870	875
Tyr Tyr Asp Glu Gln Ile	Tyr Gly Phe Lys Val Asn Leu Lys Pro Glu	880
885	890	895
Lys Lys Ser Lys Leu Val Ser Val Val Ser Arg Ile Arg Gly His Asp		
900	905	910
Gln Asp Thr Gly Arg Gln Gln Val Thr Gly Gly Lys Leu Arg Glu Ile		
915	920	925
Gln Asp Glu Ala Lys Ser Phe Ala Ile Gly Asn Lys Pro Leu Ala Ala		
930	935	940
Leu Phe Val His Thr Pro Ala Gly Glu Leu Gln Arg Gln Ile Arg Ser		
945	950	955
Trp Leu Ala Glu Ser Phe Glu Phe Leu Ser Val Thr Ala Asp Asp Val		
965	970	975
Ser Gly Val Thr Thr Gly Gln Leu Glu Leu Ser Thr Ala Ile Met		
980	985	990
Asp Gly Trp Met Ala Gly Val Gly Ala Ala Val Pro Pro His Thr Asp		
995	1000	1005
Ala Leu Gly Gln Leu Leu Ser Glu Tyr Ala Lys Arg Val Tyr Thr		
1010	1015	1020
Ser Gln Met Gln His Leu Lys Asp Ile Ala Gly Thr Leu Ala Ser		
1025	1030	1035
Glu Glu Ala Glu Asp Ala Gly Gln Val Ala Lys Leu Arg Ser Ala		
1040	1045	1050
Leu Glu Ser Val Asp His Lys Arg Arg Lys Ile Leu Gln Gln Met		
1055	1060	1065
Arg Ser Asp Ala Ala Leu Phe Thr Leu Glu Glu Gly Ser Ser Pro		
1070	1075	1080
Val Gln Asn Pro Ser Thr Ala Ala Glu Asp Ser Arg Leu Ala Ser		
1085	1090	1095
Leu Ile Ser Leu Asp Ala Ile Leu Lys Gln Val Lys Glu Ile Thr		
1100	1105	1110
Arg Gln Ala Ser Val His Val Leu Ser Lys Ser Lys Lys Lys Ala		
1115	1120	1125
Leu Leu Glu Ser Leu Asp Glu Leu Asn Glu Arg Met Pro Ser Leu		
1130	1135	1140
Leu Asp Val Asp His Pro Cys Ala Gln Arg Glu Ile Asp Thr Ala		
1145	1150	1155
His Gln Leu Val Glu Thr Ile Pro Glu Gln Glu Asp Asn Leu Gln		
1160	1165	1170
Asp Glu Lys Arg Pro Ser Ile Asp Ser Ile Ser Ser Thr Glu Thr		
1175	1180	1185
Asp Val Ser Gln Trp Asn Val Leu Gln Phe Asn Thr Gly Gly Ser		
1190	1195	1200
Ser Ala Pro Phe Ile Ile Lys Cys Gly Ala Asn Ser Asn Ser Glu		
1205	1210	1215
Leu Val Ile Lys Ala Asp Ala Arg Ile Gln Glu Pro Lys Gly Gly		
1220	1225	1230
Glu Ile Val Arg Val Val Pro Arg Pro Ser Val Leu Glu Asn Met		
1235	1240	1245
Ser Leu Glu Glu Met Lys Gln Val Phe Gly Gln Leu Pro Glu Ala		
1250	1255	1260
Leu Ser Ser Leu Ala Leu Ala Arg Thr Ala Asp Gly Thr Arg Ala		
1265	1270	1275
Arg Tyr Ser Arg Leu Tyr Arg Thr Leu Ala Met Lys Val Pro Ser		
1280	1285	1290

Leu Arg Asp Leu Val Gly Glu Leu Glu Lys Gly Gly Val Leu Lys
 1295 1300 1305
 Asp Thr Lys Ser Thr
 1310

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 <212> PRT
 <213> Arabidopsis thaliana

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 20 25 30
 Asn Asn Asn Pro Pro Thr Met Thr Arg Ser Asp Pro Arg Leu Asp His
 35 40 45
 Asp Phe Thr Thr Asn Asn Ser Gly Ser Pro Asn Thr Gln Thr Gln Ser
 50 55 60
 Gln Glu Glu Gln Asn Ser Arg Asp Glu Gln Pro Ala Val Glu Pro Gly
 65 70 75 80
 Ser Gly Ser Gly Ser Thr Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly
 85 90 95
 Ser Lys Asn Lys Pro Lys Ser Pro Val Val Thr Lys Glu Ser Pro
 100 105 110
 Asn Ser Leu Gln Ser His Val Leu Glu Ile Ala Thr Gly Ala Asp Val
 115 120 125
 Ala Glu Ser Leu Asn Ala Phe Ala Arg Arg Arg Gly Arg Gly Val Ser
 130 135 140
 Val Leu Ser Gly Ser Gly Leu Val Thr Asn Val Thr Leu Arg Gln Pro
 145 150 155 160
 Ala Ala Ser Gly Gly Val Val Ser Leu Arg Gly Gln Phe Glu Ile Leu
 165 170 175
 Ser Met Cys Gly Ala Phe Leu Pro Thr Ser Gly Ser Pro Ala Ala Ala
 180 185 190
 Ala Gly Leu Thr Ile Tyr Leu Ala Gly Ala Gln Gly Gln Val Val Gly
 195 200 205
 Gly Gly Val Ala Gly Pro Leu Ile Ala Ser Gly Pro Val Ile Val Ile
 210 215 220
 Ala Ala Thr Phe Cys Asn Ala Thr Tyr Glu Arg Leu Pro Ile Glu Glu
 225 230 235 240
 Glu Gln Gln Gln Glu Gln Pro Leu Gln Leu Glu Asp Gly Lys Lys Gln
 245 250 255
 Lys Glu Glu Asn Asp Asp Asn Glu Ser Gly Asn Asn Gly Asn Glu Gly
 260 265 270
 Ser Met Gln Pro Pro Met Tyr Asn Met Pro Pro Asn Phe Ile Pro Asn
 275 280 285
 Gly His Gln Met Ala Gln His Asp Val Tyr Trp Gly Gly Pro Pro Pro
 290 295 300
 Arg Ala Pro Pro Ser Tyr
 305 310

<210> 123
 <211> 964
 <212> PRT

<213> Arabidopsis thaliana

<400> 123

Met 1	Ala	Leu	Asn	Leu	Arg	Gln	Lys	Gln	Thr	Glu	Cys	Val	Ile	Arg	Met
Leu	Asn	Leu	Asn	Gln	Pro	Leu	Asn	Pro	Ser	Gly	Thr	Ala	Asn	Glu	Glu
Val	Tyr	Lys	Ile	Leu	Ile	Tyr	Asp	Arg	Phe	Cys	Gln	Asn	Ile	Leu	Ser
Pro	Leu	Thr	His	Val	Lys	Asp	Leu	Arg	Lys	His	Gly	Val	Thr	Leu	Phe
Phe	Leu	Ile	Asp	Lys	Asp	Arg	Gln	Pro	Val	His	Asp	Val	Pro	Ala	Val
Tyr	Phe	Val	Gln	Pro	Thr	Glu	Ser	Asn	Leu	Gln	Arg	Ile	Ile	Ala	Asp
Ala	Ser	Arg	Ser	Leu	Tyr	Asp	Thr	Phe	His	Leu	Asn	Phe	Ser	Ser	Ser
Ile	Pro	Arg	Lys	Phe	Leu	Glu	Glu	Leu	Ala	Ser	Gly	Thr	Leu	Lys	Ser
Gly	Ser	Val	Glu	Lys	Val	Ser	Lys	Val	His	Asp	Gln	Tyr	Leu	Glu	Phe
Val	Thr	Leu	Glu	Asp	Asn	Leu	Phe	Ser	Leu	Ala	Gln	Gln	Ser	Thr	Tyr
Val	Gln	Met	Asn	Asp	Pro	Ser	Ala	Gly	Glu	Lys	Glu	Ile	Asn	Glu	Ile
Ile	Glu	Arg	Val	Ala	Ser	Gly	Leu	Phe	Cys	Val	Leu	Val	Thr	Leu	Gly
Val	Val	Pro	Val	Ile	Arg	Cys	Pro	Ser	Gly	Gly	Pro	Ala	Glu	Met	Val
Ala	Ser	Leu	Leu	Asp	Gln	Lys	Leu	Arg	Asp	His	Leu	Ser	Lys	Asn	
Asn	Leu	Phe	Thr	Glu	Gly	Gly	Gly	Phe	Met	Ser	Ser	Phe	Gln	Arg	Pro
Leu	Leu	Cys	Ile	Phe	Asp	Arg	Asn	Phe	Glu	Leu	Ser	Val	Gly	Ile	Gln
His	Asp	Phe	Arg	Tyr	Arg	Pro	Leu	Val	His	Asp	Val	Leu	Gly	Leu	Lys
Leu	Asn	Gln	Leu	Lys	Val	Gln	Gly	Glu	Lys	Gly	Pro	Pro	Lys	Ser	Phe
Glu	Leu	Asp	Ser	Ser	Asp	Pro	Phe	Trp	Ser	Ala	Asn	Ser	Thr	Leu	Glu
Phe	Pro	Asp	Val	Ala	Val	Glu	Ile	Glu	Thr	Gln	Leu	Asn	Lys	Tyr	Lys
Arg	Asp	Val	Glu	Glu	Val	Asn	Lys	Lys	Thr	Gly	Gly	Gly	Ser	Gly	Ala
Glu	Phe	Asp	Gly	Thr	Asp	Leu	Ile	Gly	Asn	Ile	His	Thr	Glu	His	Leu
Met	Asn	Thr	Val	Lys	Ser	Leu	Pro	Glu	Leu	Thr	Glu	Arg	Lys	Lys	Val
Ile	Asp	Lys	His	Thr	Asn	Ile	Ala	Thr	Ala	Leu	Leu	Gly	Gln	Ile	Lys
Glu	Arg	Ser	Ile	Asp	Ala	Phe	Thr	Lys	Lys	Glu	Ser	Asp	Met	Met	Met
Arg	Gly	Gly	Ile	Asp	Arg	Thr	Glu	Leu	Met	Ala	Ala	Leu	Lys	Gly	Lys
Gly	Thr	Lys	Met	Asp	Lys	Leu	Arg	Phe	Ala	Ile	Met	Tyr	Leu	Ile	Ser

Thr	Glu	Thr	Ile	Asn	Gln	Ser	Glu	Val	Glu	Ala	Val	Glu	Ala	Ala	Leu
	435						440					445			
Asn	Glu	Ala	Glu	Ala	Asp	Thr	Ser	Ala	Phe	Gln	Tyr	Val	Lys	Lys	Ile
	450					455					460				
Lys	Ser	Leu	Asn	Ala	Ser	Phe	Ala	Ala	Thr	Ser	Ala	Asn	Ser	Ala	Ser
465					470					475					480
Arg	Ser	Asn	Ile	Val	Asp	Trp	Ala	Glu	Lys	Leu	Tyr	Gly	Gln	Ser	Ile
			485						490					495	
Ser	Ala	Val	Thr	Ala	Gly	Val	Lys	Asn	Leu	Leu	Ser	Ser	Asp	Gln	Gln
		500						505					510		
Leu	Ala	Val	Thr	Arg	Thr	Val	Glu	Ala	Leu	Thr	Glu	Gly	Lys	Pro	Asn
	515						520					525			
Pro	Glu	Ile	Asp	Ser	Tyr	Arg	Phe	Leu	Asp	Pro	Arg	Ala	Pro	Lys	Ser
	530					535					540				
Ser	Ser	Ser	Gly	Gly	Ser	His	Val	Lys	Gly	Pro	Phe	Arg	Glu	Ala	Ile
545					550					555					560
Val	Phe	Met	Ile	Gly	Gly	Gly	Asn	Tyr	Val	Glu	Tyr	Gly	Ser	Leu	Gln
			565						570					575	
Glu	Leu	Thr	Gln	Arg	Gln	Leu	Thr	Val	Lys	Asn	Val	Ile	Tyr	Gly	Ala
		580						585				590			
Thr	Glu	Ile	Leu	Asn	Gly	Gly	Glu	Leu	Val	Glu	Gln	Leu	Gly	Leu	Leu
	595						600					605			
Gly	Lys	Lys	Met	Gly	Leu	Gly	Gly	Pro	Val	Ala	Ser	Thr	Leu	Lys	Arg
	610				615						620				
Leu	Gly	Met	Ala	Gly	Lys	Glu	Glu	Thr	Asp	Val	Ser	Ala	Gln	Gly	Ser
625					630					635					640
Leu	Thr	Arg	Glu	Ala	Thr	Glu	Ile	Trp	Arg	Ser	Glu	Leu	Glu	Ser	Arg
			645					650						655	
Arg	Phe	Gln	Val	Asp	Ser	Leu	Glu	Ala	Glu	Leu	Val	Asp	Val	Lys	Ala
		660						665				670			
Tyr	Leu	Glu	Phe	Gly	Ser	Glu	Glu	Asp	Ala	Arg	Lys	Glu	Leu	Gly	Val
	675					680					685				
Leu	Ser	Gly	Arg	Val	Arg	Ser	Thr	Ala	Thr	Met	Leu	Arg	Tyr	Leu	Arg
	690				695						700				
Ser	Lys	Ala	Arg	Val	Leu	Ala	Ile	Pro	Asp	Asp	Leu	Ala	Asn	Val	Ser
705					710					715					720
Cys	Gly	Val	Glu	Gln	Ile	Glu	Glu	Leu	Lys	Gly	Leu	Asn	Leu	Val	Glu
			725						730					735	
Lys	Asp	Gly	Gly	Ser	Ser	Ser	Ser	Asp	Gly	Ala	Arg	Asn	Thr	Asn	Pro
		740						745				750			
Glu	Thr	Arg	Arg	Tyr	Ser	Gly	Ser	Leu	Gly	Val	Glu	Asp	Gly	Ala	Tyr
	755					760					765				
Thr	Asn	Glu	Met	Leu	Gln	Ser	Ile	Glu	Met	Val	Thr	Asp	Val	Leu	Asp
	770				775						780				
Ser	Leu	Val	Arg	Arg	Val	Thr	Val	Ala	Glu	Ser	Glu	Ser	Ala	Val	Gln
785					790					795					800
Lys	Glu	Arg	Ala	Leu	Leu	Gly	Glu	Glu	Glu	Ile	Ser	Arg	Lys	Thr	Ile
			805						810					815	
Gln	Ile	Glu	Asn	Leu	Ser	Val	Lys	Leu	Glu	Glu	Met	Glu	Arg	Phe	Ala
		820						825				830			
Tyr	Gly	Thr	Asn	Ser	Val	Leu	Asn	Glu	Met	Arg	Glu	Arg	Ile	Glu	Glu
	835					840					845				
Leu	Val	Glu	Glu	Thr	Met	Arg	Gln	Arg	Glu	Lys	Ala	Val	Glu	Asn	Glu
	850				855					860					
Glu	Glu	Leu	Cys	Arg	Val	Lys	Arg	Glu	Phe	Glu	Ser	Leu	Lys	Ser	Tyr
865					870					875					880
Val	Ser	Thr	Phe	Thr	Asn	Val	Arg	Glu	Thr	Leu	Leu	Ser	Ser	Glu	Arg

				885					890					895			
Gln	Phe	Lys	Thr	Ile	Glu	Glu	Leu	Phe	Glu	Arg	Leu	Val	Thr	Lys	Thr		
			900						905					910			
Thr	Gln	Leu	Glu	Gly	Glu	Lys	Ala	Gln	Lys	Glu	Val	Glu	Val	Gln	Lys		
		915					920						925				
Leu	Met	Glu	Glu	Asn	Val	Lys	Leu	Thr	Ala	Leu	Leu	Asp	Lys	Lys	Glu		
	930					935						940					
Ala	Gln	Leu	Leu	Ala	Leu	Asn	Glu	Gln	Cys	Lys	Val	Met	Ala	Leu	Ser		
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Ala	Ser	Asn	Ile														

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 Pro Gln Gly Asn Arg Leu Asp Lys Gln Glu Phe Thr Glu Leu Val Lys
 35 40 45
 Arg Gly Ser Thr Ala Glu Asp Leu Gly Ala Gly Asn Ala Asp Ala Val
 50 55 60
 Trp Val His Gly Leu Gly Tyr Ala Lys Ala Pro Arg Pro Trp Glu Asp
 65 70 75 80
 Pro Ser Thr Leu Ala Ser Ser Gln Lys Glu Asp Ala Asp Ser Ala Arg
 85 90 95
 Leu Pro Ala Asp Thr Ser Gly Val Lys Thr Val Glu Asp Gly Pro Asp
 100 105 110
 Asp Val Glu Arg Asp Gln Arg Arg Ile Gly Val Arg Lys Gly Asn Leu
 115 120 125
 Gln Arg Glu Arg Arg Lys Lys Asp Met Ile Gly Val Lys Asn Ala Lys
 130 135 140
 Gly Met Arg Ser Glu Ala Leu Val Ile Gln Met Ile Glu Arg Ser Thr
 145 150 155 160
 Arg Lys Arg Arg Arg Arg Lys Lys Glu Gly Met Thr Leu Ile Leu Ile
 165 170 175
 Glu Ala Asn Cys Pro Arg Met Glu His Phe Ala Leu Gln Arg Lys Ser
 180 185 190
 Gly Arg Leu Gly Thr Lys Ile Gln Leu Pro Leu Leu Gln Asp Leu Asn
 195 200 205
 Leu Leu Leu Ile Ser Phe Thr Asn Arg Gly Val Lys Cys Cys
 210 215 220

<210> 125
 <211> 148
 <212> PRT
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Ala Phe Met Leu Phe Asp Thr Asp Gly Asp Gly Lys Ile Ala Pro Ser
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 Glu Leu Gly Ile Leu Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala
 35 40 45
 Gln Leu Lys Ser Ile Ile Ala Ser Glu Asn Leu Ser Ser Pro Phe Asp
 50 55 60
 Phe Asn Arg Phe Leu Asp Leu Met Ala Lys His Leu Lys Thr Glu Pro
 65 70 75 80
 Phe Asp Arg Gln Leu Arg Asp Ala Phe Lys Val Leu Asp Lys Glu Gly
 85 90 95
 Thr Gly Phe Val Ala Val Ala Asp Leu Arg His Ile Leu Thr Ser Ile
 100 105 110
 Gly Glu Lys Leu Glu Pro Asn Glu Phe Asp Glu Trp Ile Lys Glu Val
 115 120 125
 Asp Val Gly Ser Asp Gly Lys Ile Arg Tyr Glu Asp Phe Ile Ala Arg
 130 135 140
 Met Val Ala Lys
 145

<210> 126
 <211> 70
 <212> PRT
 <213> Arabidopsis thaliana

<400> 126
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 Leu Leu Asn Cys Val Ala Glu Ser Pro Phe Asp Gln Glu Lys Cys Val
 20 25 30
 Arg Phe Leu Gln Ser Leu Arg Glu Cys Val Leu Ser Lys Lys Val Lys
 35 40 45
 Lys Phe Ser Ile Pro Ser Gln Asp His Asp Ser Glu Gly Ala Ala Ser
 50 55 60
 Ala Thr Lys Arg Pro Ser
 65 70

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 <211> 385
 <212> PRT
 <213> Arabidopsis thaliana

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 Asn Asn Asn Asn Asn Pro Ser Thr Arg Ser Trp Gly Thr Ala Val Ser
 20 25 30
 Gly Gln Ser Val Ser Thr Ser Gly Ser Met Gly Ser Pro Ser Ser Arg
 35 40 45
 Ser Glu Gln Thr Ile Thr Val Val Thr Ser Thr Ser Asp Thr Thr Phe
 50 55 60
 Gln Arg Leu Asn Asn Leu Asp Ile Gln Gly Asp Asp Ala Gly Ser Gln
 65 70 75 80
 Gly Ala Ser Gly Val Lys Lys Lys Lys Arg Gly Gln Arg Ala Ala Gly
 85 90 95
 Pro Asp Lys Thr Gly Arg Gly Leu Arg Gln Phe Ser Met Lys Val Cys

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Glu	Leu	Val	Ala	Glu	Phe	Ala	Leu	Pro	Asn	Asn	Asp	Gly	Thr	Ser	Pro																	
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Asp	Gln	Gln	Gln	Tyr	Asp	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Val	Tyr	Asp																	
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Ala	Leu	Asn	Val	Leu	Met	Ala	Met	Asp	Ile	Ile	Ser	Lys	Asp	Lys	Lys																	
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Glu	Ile	Gln	Trp	Arg	Gly	Leu	Pro	Arg	Thr	Ser	Leu	Ser	Asp	Ile	Glu																	
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Thr	Ala	Tyr	Ser	Gln	Glu	Leu	Glu	Glu	Gln	Tyr	Val	Gly	Leu	Gln	Asn																	
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225													230								235								240			
Gly	Gly	Val	Ala	Leu	Pro	Phe	Ile	Leu	Val	Gln	Thr	Arg	Pro	His	Ala																	
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Thr	Val	Glu	Val	Glu	Ile	Ser	Glu	Asp	Met	Gln	Leu	Val	His	Phe	Asp																	
												260								265								270				
Phe	Asn	Ser	Thr	Pro	Phe	Glu	Leu	His	Asp	Asp	Asn	Phe	Val	Leu	Lys																	
												275								280								285				
Thr	Met	Lys	Phe	Cys	Asp	Gln	Pro	Pro	Gln	Gln	Pro	Asn	Gly	Arg	Asn																	
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Asn	Ser	Gln	Leu	Val	Cys	His	Asn	Phe	Thr	Pro	Glu	Asn	Pro	Asn	Lys																	
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Gly	Pro	Ser	Thr	Gly	Pro	Thr	Pro	Gln	Leu	Asp	Met	Tyr	Glu	Thr	His																	
												325								330								335				
Leu	Gln	Ser	Gln	Gln	His	Gln	Gln	His	Ser	Gln	Leu	Gln	Ile	Ile	Pro																	
												340								345								350				
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Lys	Ser	Pro	Ser	Leu	Pro	Gly	Ile	Met	Asn	Ser	Ser	Met	Lys	Pro	Glu																	
												370								375								380				
																												Asn				
																												385				

Lys Phe Val Gln Cys Tyr Gly Cys Gly Asn Pro Glu Thr Glu Ile Ile
 100 105 110
 Ile Thr Lys Thr Gln Met Val Asn Leu Lys Cys Ala Ala Cys Gly Phe
 115 120 125
 Ile Ser Glu Val Asp Met Arg Asp Lys Leu Thr Asn Phe Ile Leu Lys
 130 135 140
 Asn Pro Pro Glu Gln Lys Lys Val Ser Lys Asp Lys Lys Ala Met Arg
 145 150 155 160
 Lys Ala Glu Lys Glu Arg Leu Lys Glu Gly Glu Leu Ala Asp Glu Glu
 165 170 175
 Gln Arg Lys Leu Lys Ala Lys Lys Lys Ala Leu Ser Asn Gly Lys Asp
 180 185 190
 Ser Lys Thr Ser Lys Asn His Ser Ser Asp Glu Asp Ile Ser Pro Lys
 195 200 205
 His Asp Glu Asn Ala Leu Glu Val Asp Glu Asp Glu Asp Asp Asp
 210 215 220
 Gly Val Glu Trp Gln Thr Asp Thr Ser Arg Glu Ala Ala Glu Lys Arg
 225 230 235 240
 Met Met Glu Gln Leu Ser Ala Lys Thr Ala Glu Met Val Met Leu Ser
 245 250 255
 Ala Met Glu Val Glu Glu Lys Lys Ala Pro Lys Ser Lys Ser Asn Gly
 260 265 270
 Asn Val Val Lys Thr Glu Asn Pro Pro Pro Gln Glu Lys Asn Leu Val
 275 280 285
 Gln Asp Met Lys Glu Tyr Leu Lys Lys Gly Ser Pro Ile Ser Ala Leu
 290 295 300
 Lys Ser Phe Ile Ser Ser Leu Ser Glu Pro Pro Gln Asp Ile Met Asp
 305 310 315 320
 Ala Leu Phe Asn Ala Leu Phe Asp Gly Val Gly Lys Gly Phe Ala Lys
 325 330 335
 Glu Val Thr Lys Lys Lys Asn Tyr Leu Ala Ala Ala Ala Thr Met Gln
 340 345 350
 Glu Asp Gly Ser Gln Met His Leu Leu Asn Ser Ile Gly Thr Phe Cys
 355 360 365
 Gly Lys Asn Gly Asn Glu Glu Ala Leu Lys Glu Val Ala Leu Val Leu
 370 375 380
 Lys Ala Leu Tyr Asp Gln Asp Ile Ile Glu Glu Glu Val Val Leu Asp
 385 390 395 400
 Trp Tyr Glu Lys Gly Leu Thr Gly Ala Asp Lys Ser Ser Pro Val Trp
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 Phe Ile Leu Leu Asn Ser Leu Phe Ser Tyr Phe Ile Leu Arg Phe Ala

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Cys	Asp	Asp	His	Ala	Leu	Gln	Leu	His	Ser	Lys	Pro	Val	Glu	Glu	Ser
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Asn	Cys	Gly	Phe	Gly	Glu	Phe	His	Asn	Asp	Leu	Val	His	Arg	Gly	Cys
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Cys	Val	Glu	Lys	Ile	Ser	Ser	Ser	Leu	Cys	Ala	Pro	Ile	Glu	Ser	Asp
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Phe	Gly	Asn	Leu	Asp	Tyr	Pro	Ile	Gly	Asp	Glu	Gly	Gln	Ile	Tyr	Asn
	130					135					140				
Gly	Leu	Lys	Phe	Pro	Arg	Ser	Ile	Phe	Val	Phe	Glu	Glu	Glu	Lys	Val
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Gly	Ser	Val	Asn	Leu	Asn	Asp	Ser	Gln	Glu	Glu	Thr	Glu	Glu	Lys	Lys
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Val	Pro	Gln	Ser	His	Glu	Lys	Leu	Glu	Asp	Asp	Asp	Val	Asp	Glu	Glu
		180						185					190		
Phe	Ser	Cys	Tyr	Val	Ser	Ser	Phe	Asp	Cys	Lys	Asn	Lys	Glu	Ile	Ala
		195					200					205			
Thr	Glu	Lys	Glu	Glu	Glu	Asn	Arg	Val	Asp	Leu	Pro	Ile	Glu	Val	Glu
	210					215					220				
Thr	Ala	Glu	Ser	Ala	Pro	Lys	Asn	Leu	Glu	Phe	Tyr	Ile	Asp	Glu	Glu
225					230					235				240	
Asp	Cys	His	Leu	Ile	Pro	Val	Glu	Phe	Tyr	Lys	Pro	Ser	Glu	Glu	Val
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Arg	Glu	Ile	Ser	Asp	Ile	Asn	Gly	Asp	Phe	Ile	Leu	Asp	Phe	Gly	Val
		260					265						270		
Glu	His	Asp	Phe	Thr	Ala	Ala	Ala	Glu	Thr	Glu	Glu	Ile	Ser	Asp	Phe
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	290					295					300				
Ala	Ser	Glu	Met	Glu	Asn	Asp	Asp	Glu	Glu	Thr	Asp	Ala	Glu	Val	Ser
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Ile	Gly	Thr	Glu	Ile	Pro	Asp	His	Glu	Gln	Ile	Gly	Asp	Ile	Pro	Ser
				325					330					335	
His	Gln	Leu	Ile	Pro	His	His	Asp	Asp	Asp	Asp	His	Glu	Glu	Glu	Thr
		340					345					350			
Leu	Glu	Phe	Lys	Thr	Val	Thr	Ile	Glu	Thr	Lys	Met	Pro	Val	Leu	Asn
		355					360					365			
Ile	Asn	Glu	Glu	Arg	Ile	Leu	Glu	Ala	Gln	Gly	Ser	Met	Glu	Ser	Ser
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His	Ser	Ser	Leu	His	Asn	Ala	Met	Phe	His	Leu	Glu	Gln	Arg	Val	Ser
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Val	Asp	Gly	Ile	Glu	Cys	Pro	Glu	Gly	Val	Leu	Thr	Val	Asp	Lys	Leu
				405					410					415	
Lys	Phe	Glu	Leu	Gln	Glu	Glu	Arg	Lys	Ala	Leu	His	Ala	Leu	Tyr	Glu
		420					425						430		
Glu	Leu	Glu	Val	Glu	Arg	Asn	Ala	Ser	Ala	Val	Ala	Ala	Ser	Glu	Thr
		435					440					445			
Met	Ala	Met	Ile	Asn	Arg	Leu	His	Glu	Glu	Lys	Ala	Ala	Met	Gln	Met
	450					455					460				
Glu	Ala	Leu	Gln	Tyr	Gln	Arg	Met	Met	Glu	Glu	Gln	Ala	Glu	Phe	Asp
465					470					475				480	
Gln	Glu	Ala	Leu	Gln	Leu	Leu	Asn	Glu	Leu	Met	Val	Asn	Arg	Glu	Lys
				485					490					495	

Glu Asn Ala Glu Leu Glu Lys Glu Leu Glu Val Tyr Arg Lys Arg Met
 500 505 510
 Glu Glu Tyr Glu Ala Lys Glu Lys Met Gly Met Leu Arg Arg Arg Leu
 515 520 525
 Arg Asp Ser Ser Val Asp Ser Tyr Arg Asn Asn Gly Asp Ser Asp Glu
 530 535 540
 Asn Ser Asn Gly Glu Leu Gln Phe Lys Asn Val Glu Gly Val Thr Asp
 545 550 555 560
 Trp Lys Tyr Arg Glu Asn Glu Met Glu Asn Thr Pro Val Asp Val Val
 565 570 575
 Leu Arg Leu Asp Glu Cys Leu Asp Asp Tyr Asp Gly Glu Arg Leu Ser
 580 585 590
 Ile Leu Gly Arg Leu Lys Phe Leu Glu Glu Lys Leu Thr Asp Leu Asn
 595 600 605
 Asn Glu Glu Asp Asp Glu Glu Glu Ala Lys Thr Phe Glu Ser Asn Gly
 610 615 620
 Ser Ile Asn Gly Asn Glu His Ile His Gly Lys Glu Thr Asn Gly Lys
 625 630 635 640
 His Arg Val Ile Lys Ser Lys Arg Leu Leu Pro Leu Phe Asp Ala Val
 645 650 655
 Asp Gly Glu Met Glu Asn Gly Leu Ser Asn Gly Asn His His Glu Asn
 660 665 670
 Gly Phe Asp Asp Ser Glu Lys Gly Glu Asn Val Thr Ile Glu Glu Glu
 675 680 685
 Val Asp Glu Leu Tyr Glu Arg Leu Glu Ala Leu Glu Ala Asp Arg Glu
 690 695 700
 Phe Leu Arg His Cys Val Gly Ser Leu Lys Lys Gly Asp Lys Gly Val
 705 710 715 720
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 Asn Ile Val Lys Asn Leu Thr Ser Ser Gly Asp His Asp Lys Ile Ser
 35 40 45
 Lys Val Ile Glu Met Leu Ile Lys Glu Phe Ala Lys Ser Pro Gln Ala
 50 55 60
 Asn His Arg Lys Gly Gly Leu Ile Gly Leu Ala Ala Val Thr Val Gly
 65 70 75 80
 Leu Ser Thr Glu Ala Ala Gln Tyr Leu Glu Gln Ile Val Pro Pro Val
 85 90 95
 Ile Asn Ser Phe Ser Asp Gln Asp Ser Arg Val Arg Tyr Tyr Ala Cys
 100 105 110
 Glu Ala Leu Tyr Asn Ile Ala Lys Val Val Arg Gly Asp Phe Ile Ile
 115 120 125
 Phe Phe Asn Lys Ile Phe Asp Ala Leu Cys Lys Leu Ser Ala Asp Ser

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Asp Ile Val Thr Glu Ser Asp Gln Phe Ser Ile Glu Glu Phe Ile Pro		
165	170	175
Leu Leu Lys Glu Arg Met Asn Val Leu Asn Pro Tyr Val Arg Gln Phe		
180	185	190
Leu Val Gly Trp Ile Thr Val Leu Asp Ser Val Pro Asp Ile Asp Met		
195	200	205
Leu Gly Phe Leu Pro Asp Phe Leu Asp Gly Leu Phe Asn Met Leu Ser		
210	215	220
Asp Ser Ser His Glu Ile Arg Gln Gln Ala Asp Ser Ala Leu Ser Glu		
225	230	235
Phe Leu Gln Glu Ile Lys Asn Ser Pro Ser Val Asp Tyr Gly Arg Met		
245	250	255
Ala Glu Ile Leu Val Gln Arg Ala Ala Ser Pro Asp Glu Phe Thr Arg		
260	265	270
Leu Thr Ala Ile Thr Trp Ile Asn Glu Phe Val Lys Leu Gly Gly Asp		
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Gln Leu Val Arg Tyr Tyr Ala Asp Ile Leu Gly Ala Ile Leu Pro Cys		
290	295	300
Ile Ser Asp Lys Glu Glu Lys Ile Arg Val Val Ala Arg Glu Thr Asn		
305	310	315
Glu Glu Leu Arg Ser Ile His Val Glu Pro Ser Asp Gly Phe Asp Val		
325	330	335
Gly Ala Ile Leu Ser Val Ala Arg Arg Gln Leu Ser Ser Glu Phe Glu		
340	345	350
Ala Thr Arg Ile Glu Ala Leu Asn Trp Ile Ser Thr Leu Leu Asn Lys		
355	360	365
His Arg Thr Glu Val Leu Cys Phe Leu Asn Asp Ile Phe Asp Thr Leu		
370	375	380
Leu Lys Ala Leu Ser Asp Ser Ser Asp Asp Val Val Leu Leu Val Leu		
385	390	395
Glu Val His Ala Gly Val Ala Lys Asp Pro Gln His Phe Arg Gln Leu		
405	410	415
Ile Val Phe Leu Val His Asn Phe Arg Ala Asp Asn Ser Leu Leu Glu		
420	425	430
Arg Gly Ala Leu Ile Val Arg Arg Met Cys Val Leu Leu Asp Ala Glu		
435	440	445
Arg Val Tyr Arg Glu Leu Ser Thr Ile Leu Glu Gly Glu Asp Asn Leu		
450	455	460
Asp Phe Ala Ser Thr Met Val Gln Ala Leu Asn Leu Ile Leu Leu Thr		
465	470	475
Ser Pro Glu Leu Ser Lys Leu Arg Glu Leu Leu Lys Gly Ser Leu Val		
485	490	495
Asn Arg Glu Gly Lys Glu Leu Phe Val Ala Leu Tyr Thr Ser Trp Cys		
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His Ser Pro Met Ala Ile Ile Ser Leu Cys Leu Leu Ala Gln Ala Tyr		
515	520	525
Gln His Ala Ser Val Val Ile Gln Ser Leu Val Glu Glu Asp Ile Asn		
530	535	540
Val Lys Phe Leu Val Gln Leu Asp Lys Leu Ile Arg Leu Leu Glu Thr		
545	550	555
Pro Ile Phe Thr Tyr Leu Arg Leu Gln Leu Leu Glu Pro Gly Arg Tyr		
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Thr Trp Leu Leu Lys Thr Leu Tyr Gly Leu Leu Met Leu Leu Pro Gln		
580	585	590

Gln Ser Ala Ala Phe Lys Ile Leu Arg Thr Arg Leu Lys Thr Val Pro
 595 600 605
 Thr Tyr Ser Phe Ser Thr Gly Asn Gln Ile Gly Arg Ala Thr Ser Gly
 610 615 620
 Val Pro Phe Ser Gln Tyr Lys His Gln Asn Glu Asp Gly Asp Leu Glu
 625 630 635 640
 Asp Asp Asn Ile Asn Ser Ser His Gln Gly Ile Asn Phe Ala Val Arg
 645 650 655
 Leu Gln Gln Phe Glu Asn Val Gln Asn Leu His Arg Gly Gln Ala Arg
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 Thr Arg Val Asn Tyr Ser Tyr His Ser Ser Ser Ser Ser Thr Ser Lys
 675 680 685
 Glu Val Arg Arg Ser Glu Glu Gln Gln Gln Gln Gln Gln Gln Gln
 690 695 700
 Gln Gln Gln Gln Gln Gln Arg Pro Pro Pro Ser Ser Thr Ser Ser
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 Asp Gly Ala Glu Asn Asp Asp Ser Leu Ser Phe Gly Ser Gly Glu Ala
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 Val Ser Ala Leu Glu Arg Ser Leu Arg Leu Thr Phe Met Asp Glu Leu
 65 70 75 80
 Met Glu Arg Ala Arg Asn Arg Asp Thr Ser Gly Val Ser Glu Val Ile
 85 90 95
 Tyr Asp Met Ile Ala Ala Gly Leu Ser Pro Gly Pro Arg Ser Phe His
 100 105 110
 Gly Leu Val Val Ala His Ala Leu Asn Gly Asp Glu Gln Gly Ala Met
 115 120 125
 His Ser Leu Arg Lys Glu Leu Gly Ala Gly Gln Arg Pro Leu Pro Glu
 130 135 140
 Thr Met Ile Ala Leu Val Arg Leu Ser Gly Ser Lys Gly Asn Ala Thr
 145 150 155 160
 Arg Gly Leu Glu Ile Leu Ala Ala Met Glu Lys Leu Lys Tyr Asp Ile
 165 170 175
 Arg Gln Ala Trp Leu Ile Leu Val Glu Glu Leu Met Arg Ile Asn His
 180 185 190
 Leu Glu Asp Ala Asn Lys Val Phe Leu Lys Gly Ala Arg Gly Gly Met
 195 200 205
 Arg Ala Thr Asp Gln Leu Tyr Asp Leu Met Ile Glu Glu Asp Cys Lys
 210 215 220
 Ala Gly Asp His Ser Asn Ala Leu Asp Ile Ser Tyr Glu Met Glu Ala

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				245					250						255
Gln	Ala	Thr	Cys	Gly	Ile	Pro	Glu	Val	Ala	Tyr	Ala	Thr	Phe	Glu	Asn
			260					265						270	
Met	Glu	Tyr	Gly	Glu	Gly	Leu	Phe	Met	Lys	Pro	Asp	Thr	Glu	Thr	Tyr
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Asn	Trp	Val	Ile	Gln	Ala	Tyr	Thr	Arg	Ala	Glu	Ser	Tyr	Asp	Arg	Val
	290					295					300				
Gln	Asp	Val	Ala	Glu	Leu	Gly	Met	Met	Val	Glu	Asp	His	Lys	Arg	
305					310				315					320	
Val	Gln	Pro	Asn	Val	Lys	Thr	Tyr	Ala	Leu	Leu	Val	Glu	Cys	Phe	Thr
			325					330						335	
Lys	Tyr	Cys	Val	Val	Lys	Glu	Ala	Ile	Arg	His	Phe	Arg	Ala	Leu	Lys
			340				345						350		
Asn	Phe	Glu	Gly	Gly	Thr	Val	Ile	Leu	His	Asn	Ala	Gly	Asn	Phe	Glu
	355						360					365			
Asp	Pro	Leu	Ser	Leu	Tyr	Leu	Arg	Ala	Leu	Cys	Arg	Glu	Gly	Arg	Ile
	370					375					380				
Val	Glu	Leu	Ile	Asp	Ala	Leu	Asp	Ala	Met	Arg	Lys	Asp	Asn	Gln	Pro
385				390					395					400	
Ile	Pro	Pro	Arg	Ala	Met	Ile	Met	Ser	Arg	Lys	Tyr	Arg	Thr	Leu	Val
			405					410						415	
Ser	Ser	Trp	Ile	Glu	Pro	Leu	Gln	Glu	Glu	Ala	Glu	Leu	Gly	Tyr	Glu
			420				425						430		
Ile	Asp	Tyr	Leu	Ala	Arg	Tyr	Ile	Glu	Glu	Gly	Gly	Leu	Thr	Gly	Glu
	435					440						445			
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	450				455						460				
Ala	Ser	Gly	Phe	Ile	Tyr	Ser	Asn	Pro	Ile	Glu	Thr	Ser	Phe	Lys	Gln
465				470					475					480	
Arg	Cys	Leu	Glu	Asp	Trp	Lys	Val	His	His	Arg	Lys	Leu	Leu	Arg	Thr
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Leu	Gln	Ser	Glu	Gly	Leu	Pro	Val	Leu	Gly	Asp	Ala	Ser	Glu	Ser	Asp
			500				505						510		
Tyr	Met	Arg	Val	Val	Glu	Arg	Leu	Arg	Asn	Ile	Ile	Lys	Gly	Pro	Ala
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Leu	Asn	Leu	Leu	Lys	Pro	Lys	Ala	Ala	Ser	Lys	Met	Val	Val	Ser	Glu
	530				535						540				
Leu	Lys	Glu	Glu	Leu	Glu	Ala	Gln	Gly	Leu	Pro	Ile	Asp	Gly	Thr	Arg
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Asn	Val	Leu	Tyr	Gln	Arg	Val	Gln	Lys	Ala	Arg	Arg	Ile	Asn	Lys	Ser
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Arg	Gly	Arg	Pro	Leu	Trp	Val	Pro	Pro	Ile	Glu	Glu	Glu	Glu	Glu	Glu
			580				585						590		
Val	Asp	Glu	Glu	Val	Asp	Asp	Leu	Ile	Cys	Arg	Ile	Lys	Leu	His	Glu
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Gly	Asp	Thr	Glu	Phe	Trp	Lys	Arg	Arg	Phe	Leu	Gly	Glu	Gly	Leu	Ile
	610				615						620				
Glu	Thr	Ser	Val	Glu	Ser	Lys	Glu	Thr	Thr	Glu	Ser	Val	Val	Thr	Gly
625				630					635					640	
Glu	Ser	Glu	Lys	Ala	Ile	Glu	Asp	Ile	Ser	Lys	Glu	Ala	Asp	Asn	Glu
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Glu	Asp	Asp	Asp	Glu	Glu	Glu	Gln	Glu	Gly	Asp	Glu	Asp	Asp	Asp	Glu
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Asn	Glu	Glu	Glu	Glu	Val	Val	Val	Pro	Glu	Thr	Glu	Asn	Arg	Ala	Glu
	675					680						685			

Gly	Glu	Asp	Leu	Val	Lys	Asn	Lys	Ala	Ala	Asp	Ala	Lys	Lys	His	Leu
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Gln	Met	Ile	Gly	Val	Gln	Leu	Leu	Lys	Glu	Ser	Asp	Glu	Ala	Asn	Arg
705					710					715					720
Thr	Lys	Lys	Arg	Gly	Lys	Arg	Ala	Ser	Arg	Met	Thr	Leu	Glu	Asp	Asp
				725					730					735	
Ala	Asp	Glu	Asp	Trp	Phe	Pro	Glu	Glu	Pro	Phe	Glu	Ala	Phe	Lys	Glu
				740				745					750		
Met	Arg	Glu	Arg	Lys	Val	Phe	Asp	Val	Ala	Asp	Met	Tyr	Thr	Ile	Ala
				755			760					765			
Asp	Val	Trp	Gly	Trp	Thr	Trp	Glu	Lys	Asp	Phe	Lys	Asn	Lys	Thr	Pro
				770		775					780				
Arg	Lys	Trp	Ser	Gln	Glu	Trp	Glu	Val	Glu	Leu	Ala	Ile	Val	Leu	Met
785					790					795					800
Thr	Lys	Val	Ile	Glu	Leu	Gly	Gly	Ile	Pro	Thr	Ile	Gly	Asp	Cys	Ala
				805					810					815	
Val	Ile	Leu	Arg	Ala	Ala	Leu	Arg	Ala	Pro	Met	Pro	Ser	Ala	Phe	Leu
				820				825					830		
Lys	Ile	Leu	Gln	Thr	Thr	His	Ser	Leu	Gly	Tyr	Ser	Phe	Gly	Ser	Pro
				835			840					845			
Leu	Tyr	Asp	Glu	Ile	Ile	Thr	Leu	Cys	Leu	Asp	Leu	Gly	Glu	Leu	Asp
				850		855					860				
Ala	Ala	Ile	Ala	Ile	Val	Ala	Asp	Met	Glu	Thr	Thr	Gly	Ile	Thr	Val
865					870					875					880
Pro	Asp	Gln	Thr	Leu	Asp	Lys	Val	Ile	Ser	Ala	Arg	Gln	Ser	Asn	Glu
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<212> PRT

<213> Arabidopsis thaliana

<400> 132

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			20					25					30		
Phe	His	Tyr	Asp	Asp	Ala	Ser	Gln	Ala	Lys	Ile	Gln	Gln	Glu	Lys	Pro
			35				40					45			
Trp	Ala	Ser	Asp	Pro	Asn	Tyr	Phe	Lys	Arg	Val	His	Ile	Ser	Ala	Leu
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Ala	Leu	Leu	Lys	Met	Val	Val	His	Ala	Arg	Ser	Gly	Gly	Thr	Ile	Glu
65					70					75					80
Ile	Met	Gly	Leu	Met	Gln	Gly	Lys	Thr	Glu	Gly	Asp	Thr	Ile	Ile	Val
				85					90					95	
Met	Asp	Ala	Phe	Ala	Leu	Pro	Val	Glu	Gly	Thr	Glu	Thr	Arg	Val	Asn
				100				105					110		
Ala	Gln	Ser	Asp	Ala	Tyr	Glu	Tyr	Met	Val	Glu	Tyr	Ser	Gln	Thr	Ser
				115				120				125			
Lys	Leu	Ala	Gly	Arg	Leu	Glu	Asn	Val	Val	Gly	Trp	Tyr	His	Ser	His
							135				140				
Pro	Gly	Tyr	Gly	Cys	Trp	Leu	Ser	Gly	Ile	Asp	Val	Ser	Thr	Gln	Met
145					150					155					160
Leu	Asn	Gln	Gln	Tyr	Gln	Glu	Pro	Phe	Leu	Ala	Val	Val	Ile	Asp	Pro

															165																170																175
Thr	Arg	Thr				Val	Ser	Ala	Gly	Lys				Val	Glu	Ile	Gly	Ala	Phe	Arg	Thr																										
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Tyr	Pro	Glu	Gly	His	Lys	Ile	Ser	Asp	Asp	His	Val	Ser	Glu	Tyr	Gln																																
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Thr	Ile	Pro	Leu	Asn	Lys	Ile	Glu	Asp	Phe	Gly	Val	His	Cys	Lys	Gln																																
															210																215																220
Tyr	Tyr	Ser	Leu	Asp	Ile	Thr	Tyr	Phe	Lys	Ser	Ser	Leu	Asp	Ser	His																																
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Leu	Leu	Asp	Leu	Leu	Trp	Asn	Lys	Tyr	Trp	Val	Asn	Thr	Leu	Ser	Ser																																
															245																250																255
Ser	Pro	Leu	Leu	Gly	Asn	Gly	Asp	Tyr	Val	Ala	Gly	Gln	Ile	Ser	Asp																																
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Leu	Ala	Glu	Lys	Leu	Glu	Gln	Ala	Glu	Ser	Gln	Leu	Ala	Asn	Ser	Arg																																
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Tyr	Gly	Gly	Ile	Ala	Pro	Ala	Gly	His	Gln	Arg	Arg	Lys	Glu	Asp	Glu																																
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Pro	Gln	Leu	Ala	Lys	Ile	Thr	Arg	Asp	Ser	Ala	Lys	Ile	Thr	Val	Glu																																
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Gln	Val	His	Gly	Leu	Met	Ser	Gln	Val	Ile	Lys	Asp	Ile	Leu	Phe	Asn																																
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Ser	Ala	Arg	Gln	Ser	Lys	Lys	Ser	Ala	Asp	Asp	Ser	Ser	Asp	Pro	Glu																																
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Pro	Met	Ile	Thr	Ser																																											
															355																																

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<220>
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57

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<400> 136
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<210> 142

<211> 52

<212> DNA

<213> artificial sequence

<220>

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<211> 52

<212> DNA

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<400> 143

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<210> 145
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<400> 145
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<210> 146
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<220>

<223> Description of Artificial Sequence: primer

<400> 146
ggggaccact ttgtacaaga aagctgggtc caaaagaaga gcaacttca 49

<210> 147
<211> 56
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<223> Description of Artificial Sequence: primer

<400> 147
ggggacaagt ttgtacaaaa aagcaggctt cacaatgtat tgctcttctt cgatgc 56

<210> 148
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<210> 149
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<210> 154
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<210> 156
<211> 53
<212> DNA
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<220>
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<212> DNA

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<400> 160

ggggaccact ttgtacaaga aagctgggtt cagcgagtat caatggatc 49

<210> 161

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<210> 163

<211> 55

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 163

ggggacaagt ttgtacaaaa aagcaggctt cacaatgaat agggaaaagt tgatg 55

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52

<210> 166
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ggggaccact ttgtacaaga aagctggggtt gtcagctact tacattgccg

50

<210> 167
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ggggacaagt ttgtacaaaa aagcaggctt cacaatggcc accgtatctt c

51

<210> 168
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<210> 170
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<210> 171
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<210> 172
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ggggaccact ttgtacaaga aagctgggtt taagaggaac tagccggtg 49

<210> 173
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<210> 174

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<400> 174

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51

<210> 175

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<212> DNA

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<220>

<223> Description of Artificial Sequence: primer

<400> 175

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<210> 176

<211> 47

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<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 176

ggggaccact ttgtacaaga aagctgggta tctcaagctt taaacgc

47

<210> 177

<211> 54

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 177

ggggacaagt ttgtacaaaa aagcaggctt cacaatggcg gagcagaaga gtac

54

<210> 178

<211> 54

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<210> 179

<211> 51

<212> DNA

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<400> 179

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<210> 180

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<223> Description of Artificial Sequence: primer

<400> 180

ggggaccact ttgtacaaga aagctgggtt caatacgaag gaggagca 48

<210> 181

<211> 53

<212> DNA

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<400> 181

ggggacaagt ttgtacaaaa aagcaggctt cacaatggct ctcaatctcc gtc 53

<210> 182

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<210> 183
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<210> 184
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<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 184
ggggaccact ttgtacaaga aagctggggtt ttcaacaatg ttcaacaaca ct 52

<210> 185
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<210> 186
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ggggaccact ttgtacaaga aagctggggtt ttagtgcaac caaagagtc 49

<210> 187
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<210> 188
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<210> 189
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<400> 190
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<211> 52
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<400> 191
ggggacaagt ttgtacaaaa aagcaggctt cacaatggcg ctgcagaaca tt 52

<210> 192
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<210> 193

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<220>

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<400> 193

ggggacaagt ttgtacaaaa aagcaggctt cacaatggcg gtaacaaat tcg 53

<210> 194

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<400> 194

ggggaccact ttgtacaaga aagctgggtg tcgttgttcc ttgcctcac 49

<210> 195

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<210> 196

<211> 54

<212> DNA

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<210> 197

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<223> Description of Artificial Sequence: primer

<400> 197

ggggacaagt ttgtacaaaa aagcaggctt cacaatggaa ggctcctcgt cag 53

<210> 198

<211> 48

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 198

ggggaccact ttgtacaaga aagctggggtt cacgatgtaa tcatgggc 48

<210> 199

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 199

Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser
1 5 10

<210> 200

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 200

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 201

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 201

Asp Tyr Lys Asp Asp Asp Lys

1

5

<210> 202
 <211> 9
 <212> PRT
 <213> artificial sequence

<220>
 <223> Description of Artificial Sequence: motif

<400> 202
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> 203
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<220>
 <223> Description of Artificial Sequence: motif

<400> 203
 Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
 1 5 10

<210> 204
 <211> 11
 <212> PRT
 <213> artificial sequence

<220>
 <223> Description of Artificial Sequence: motif

<400> 204
 Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
 1 5 10

<210> 205
 <211> 131
 <212> PRT
 <213> Arabidopsis thaliana

<400> 205
 Asn Arg Ile Leu Trp Lys Gly Val Asp Ala Cys Pro Gly Asp Glu Asp
 1 5 10 15
 Ala Asp Val Ser Val Leu Gln Leu Gln Ala Glu Ile Glu Asn Leu Ala
 20 25 30
 Leu Glu Glu Gln Ala Leu Asp Asn Gln Ile Arg Gln Thr Glu Glu Arg
 35 40 45
 Leu Arg Asp Leu Ser Glu Asn Glu Lys Asn Gln Lys Trp Leu Phe Val
 50 55 60
 Thr Glu Glu Asp Ile Lys Ser Leu Pro Gly Phe Gln Asn Gln Thr Leu

65					70					75				80
Ile	Ala	Val	Lys	Ala	Pro	His	Gly	Thr	Thr	Leu	Glu	Val	Pro	Asp
				85					90					95
Asp	Glu	Ala	Ala	Asp	His	Pro	Gln	Arg	Arg	Tyr	Arg	Ile	Ile	Leu
			100					105					110	Arg
Ser	Thr	Met	Gly	Pro	Ile	Asp	Val	Tyr	Leu	Val	Ser	Glu	Phe	Glu
		115					120					125		Gly
Lys	Phe	Glu												
	130													

<210> 206
 <211> 385
 <212> PRT
 <213> Arabidopsis thaliana

<400> 206
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 His Pro Ser Leu Ser Ser Met Lys Pro Pro Leu Val Ala Pro Gly Glu
 20 25 30
 Tyr His Arg Phe Asp Ala Ala Glu Thr Arg Gly Gly Gly Ala Val Ala
 35 40 45
 Asp Gln Val Val Ser Asp Ala Ile Val Ile Lys Ser Thr Leu Lys Arg
 50 55 60
 Lys Thr Asp Leu Val Asn Gln Ile Val Glu Val Asn Glu Leu Asn Thr
 65 70 75 80
 Gly Val Leu Gln Thr Pro Val Ser Gly Lys Gly Gly Lys Ala Lys Lys
 85 90 95
 Thr Ser Arg Ser Ala Lys Ser Asn Lys Ser Gly Thr Leu Ala Ser Gly
 100 105 110
 Ser Asn Ala Gly Ser Pro Gly Asn Asn Phe Ala Gln Ala Gly Thr Cys
 115 120 125
 Arg Tyr Asp Ser Ser Leu Gly Leu Leu Thr Lys Lys Phe Ile Asn Leu
 130 135 140
 Ile Lys Gln Ala Glu Asp Gly Ile Leu Asp Leu Asn Lys Ala Ala Asp
 145 150 155 160
 Thr Leu Glu Val Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu
 165 170 175
 Glu Gly Ile Gly Leu Ile Glu Lys Thr Leu Lys Asn Arg Ile Gln Trp
 180 185 190
 Lys Gly Leu Asp Val Ser Lys Pro Gly Glu Thr Ile Glu Ser Ile Ala
 195 200 205
 Asn Leu Gln Asp Glu Val Gln Asn Leu Ala Ala Glu Glu Ala Arg Leu
 210 215 220
 Asp Asp Gln Ile Arg Glu Ser Gln Glu Arg Leu Thr Ser Leu Ser Glu
 225 230 235 240
 Asp Glu Asn Asn Lys Arg Leu Leu Phe Val Thr Glu Asn Asp Ile Lys
 245 250 255
 Asn Leu Pro Cys Phe Gln Asn Lys Thr Leu Ile Ala Val Lys Ala Pro
 260 265 270
 His Gly Thr Thr Leu Glu Val Pro Asp Pro Asp Glu Ala Gly Gly Tyr
 275 280 285
 Gln Arg Arg Tyr Arg Ile Ile Leu Arg Ser Thr Met Gly Pro Ile Asp
 290 295 300
 Val Tyr Leu Val Ser Gln Phe Glu Glu Ser Phe Glu Asp Ile Pro Gln
 305 310 315 320

Ala	Asp	Glu	Pro	Ser	Asn	Val	Pro	Asp	Glu	Pro	Ser	Asn	Val	Pro	Asp
325						330						335			
Glu	Pro	Ser	Asn	Leu	Pro	Ser	Thr	Ser	Gly	Leu	Pro	Glu	Asn	His	Asp
340						345						350			
Val	Ser	Met	Pro	Met	Lys	Glu	Glu	Ser	Thr	Glu	Arg	Asn	Met	Glu	Thr
355						360						365			
Gln	Glu	Val	Asp	Asp	Thr	Gln	Arg	Val	Tyr	Ser	Asp	Ile	Glu	Ser	His
370						375						380			
Asp															
385															

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<210> 207
<211> 127
<212> PRT
<213> Arabidopsis thaliana
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<400> 207															
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His	Pro	Ser	Leu	Ser	Ser	Met	Lys	Pro	Pro	Leu	Val	Ala	Pro	Gly	Glu
			20					25					30		
Tyr	His	Arg	Phe	Asp	Ala	Ala	Glu	Thr	Arg	Gly	Gly	Gly	Ala	Val	Ala
		35					40					45			
Asp	Gln	Val	Val	Ser	Asp	Ala	Ile	Val	Ile	Lys	Ser	Thr	Leu	Lys	Arg
	50					55					60				
Lys	Thr	Asp	Leu	Val	Asn	Gln	Ile	Val	Glu	Val	Asn	Glu	Leu	Asn	Thr
65					70					75				80	
Gly	Val	Leu	Gln	Thr	Pro	Val	Ser	Gly	Lys	Gly	Gly	Lys	Ala	Lys	Lys
				85					90					95	
Thr	Ser	Arg	Ser	Ala	Lys	Ser	Asn	Lys	Ser	Gly	Thr	Leu	Ala	Ser	Gly
			100					105					110		
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<210> 208
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<400> 208															
Met	Ser	Met	Glu	Met	Glu	Leu	Phe	Val	Thr	Pro	Glu	Lys	Gln	Arg	Gln
1				5					10					15	
His	Pro	Ser	Val	Ser	Val	Glu	Lys	Thr	Pro	Val	Arg	Arg	Lys	Leu	Ile
			20					25					30		
Val	Asp	Asp	Asp	Ser	Glu	Ile	Gly	Ser	Glu	Lys	Lys	Gly	Gln	Ser	Arg
		35					40					45			
Thr	Ser	Gly	Gly	Gly	Leu	Arg	Gln	Phe	Ser	Val	Met	Val	Cys	Gln	Lys
	50					55					60				
Leu	Glu	Ala	Lys	Lys	Ile	Thr	Thr	Tyr	Lys	Glu	Val	Ala	Asp	Glu	Ile
65					70					75					80
Ile	Ser	Asp	Phe	Ala	Thr	Ile	Lys	Gln	Asn	Ala	Glu	Lys	Pro	Leu	Asn
				85					90					95	
Glu	Asn	Glu	Tyr	Asn	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Val	Tyr	Asp	Ala
			100					105					110		
Leu	Asn	Val	Phe	Met	Ala	Leu	Asp	Ile	Ile	Ala	Arg	Asp	Lys	Lys	Glu

	115		120		125
Ile	Arg	Trp	Lys	Gly	Leu
130			135		140

<210> 209
 <211> 101
 <212> PRT
 <213> Arabidopsis thaliana

<400> 209
 Glu Lys Lys Gly Gln Ser Arg Thr Ser Gly Gly Gly Leu Arg Gln Phe
 1 5 10 15
 Ser Val Met Val Cys Gln Lys Leu Glu Ala Lys Lys Ile Thr Thr Tyr
 20 25 30
 Lys Glu Val Ala Asp Glu Ile Ile Ser Asp Phe Ala Thr Ile Lys Gln
 35 40 45
 Asn Ala Glu Lys Pro Leu Asn Glu Asn Glu Tyr Asn Glu Lys Asn Ile
 50 55 60
 Arg Arg Arg Val Tyr Asp Ala Leu Asn Val Phe Met Ala Leu Asp Ile
 65 70 75 80
 Ile Ala Arg Asp Lys Lys Glu Ile Arg Trp Lys Gly Leu Pro Ile Thr
 85 90 95
 Cys Lys Lys Asp Val
 100

<210> 210
 <211> 251
 <212> PRT
 <213> Arabidopsis thaliana

<400> 210
 Glu Lys Lys Gly Gln Ser Arg Thr Ser Gly Gly Gly Leu Arg Gln Phe
 1 5 10 15
 Ser Val Met Val Cys Gln Lys Leu Glu Ala Lys Lys Ile Thr Thr Tyr
 20 25 30
 Lys Glu Val Ala Asp Glu Ile Ile Ser Asp Phe Ala Thr Ile Lys Gln
 35 40 45
 Asn Ala Glu Lys Pro Leu Asn Glu Asn Glu Tyr Asn Glu Lys Asn Ile
 50 55 60
 Arg Arg Arg Val Tyr Asp Ala Leu Asn Val Phe Met Ala Leu Asp Ile
 65 70 75 80
 Ile Ala Arg Asp Lys Lys Glu Ile Arg Trp Lys Gly Leu Pro Ile Thr
 85 90 95
 Cys Lys Lys Asp Val Glu Glu Val Lys Met Asp Arg Asn Lys Val Met
 100 105 110
 Ser Ser Val Gln Lys Lys Ala Ala Phe Leu Lys Glu Leu Arg Glu Lys
 115 120 125
 Val Ser Ser Leu Glu Ser Leu Met Ser Arg Asn Gln Glu Met Val Val
 130 135 140
 Lys Thr Gln Gly Pro Ala Glu Gly Phe Thr Leu Pro Phe Ile Leu Leu
 145 150 155 160
 Glu Thr Asn Pro His Ala Val Val Glu Ile Glu Ile Ser Glu Asp Met
 165 170 175
 Gln Leu Val His Leu Asp Phe Asn Ser Thr Pro Phe Ser Val His Asp
 180 185 190

Asp Ala Tyr Ile Leu Lys Leu Met Gln Glu Gln Lys Gln Glu Gln Asn
 195 200 205
 Arg Val Ser Ser Ser Ser Ser Thr His His Gln Ser Gln His Ser Ser
 210 215 220
 Ala His Ser Ser Ser Ser Ser Cys Ile Ala Ser Gly Thr Ser Gly Pro
 225 230 235 240
 Val Cys Trp Asn Ser Gly Ser Ile Asp Thr Arg
 245 250

<210> 211
 <211> 172
 <212> PRT
 <213> Arabidopsis thaliana

<400> 211
 Ile Ile Ala Arg Asp Lys Lys Glu Ile Arg Trp Lys Gly Leu Pro Ile
 1 5 10 15
 Thr Cys Lys Lys Asp Val Glu Glu Val Lys Met Asp Arg Asn Lys Val
 20 25 30
 Met Ser Ser Val Gln Lys Lys Ala Ala Phe Leu Lys Glu Leu Arg Glu
 35 40 45
 Lys Val Ser Ser Leu Glu Ser Leu Met Ser Arg Asn Gln Glu Met Val
 50 55 60
 Val Lys Thr Gln Gly Pro Ala Glu Gly Phe Thr Leu Pro Phe Ile Leu
 65 70 75 80
 Leu Glu Thr Asn Pro His Ala Val Val Glu Ile Glu Ile Ser Glu Asp
 85 90 95
 Met Gln Leu Val His Leu Asp Phe Asn Ser Thr Pro Phe Ser Val His
 100 105 110
 Asp Asp Ala Tyr Ile Leu Lys Leu Met Gln Glu Gln Lys Gln Glu Gln
 115 120 125
 Asn Arg Val Ser Ser Ser Ser Ser Thr His His Gln Ser Gln His Ser
 130 135 140
 Ser Ala His Ser Ser Ser Ser Ser Cys Ile Ala Ser Gly Thr Ser Gly
 145 150 155 160
 Pro Val Cys Trp Asn Ser Gly Ser Ile Asp Thr Arg
 165 170

<210> 212
 <211> 93
 <212> PRT
 <213> Arabidopsis thaliana

<400> 212
 Ile Ile Ala Arg Asp Lys Lys Glu Ile Arg Trp Lys Gly Leu Pro Ile
 1 5 10 15
 Thr Cys Lys Lys Asp Val Glu Glu Val Lys Met Asp Arg Asn Lys Val
 20 25 30
 Met Ser Ser Val Gln Lys Lys Ala Ala Phe Leu Lys Glu Leu Arg Glu
 35 40 45
 Lys Val Ser Ser Leu Glu Ser Leu Met Ser Arg Asn Gln Glu Met Val
 50 55 60
 Val Lys Thr Gln Gly Pro Ala Glu Gly Phe Thr Leu Pro Phe Ile Leu
 65 70 75 80
 Leu Glu Thr Asn Pro His Ala Val Val Glu Ile Glu Ile

85

90

<210> 213
 <211> 121
 <212> PRT
 <213> Arabidopsis thaliana

<400> 213
 Ser Leu Glu Ser Leu Met Ser Arg Asn Gln Glu Met Val Val Lys Thr
 1 5 10 15
 Gln Gly Pro Ala Glu Gly Phe Thr Leu Pro Phe Ile Leu Leu Glu Thr
 20 25 30
 Asn Pro His Ala Val Val Glu Ile Glu Ile Ser Glu Asp Met Gln Leu
 35 40 45
 Val His Leu Asp Phe Asn Ser Thr Pro Phe Ser Val His Asp Asp Ala
 50 55 60
 Tyr Ile Leu Lys Leu Met Gln Glu Gln Lys Gln Glu Gln Asn Arg Val
 65 70 75 80
 Ser Ser Ser Ser Ser Thr His His Gln Ser Gln His Ser Ser Ala His
 85 90 95
 Ser Ser Ser Ser Ser Cys Ile Ala Ser Gly Thr Ser Gly Pro Val Cys
 100 105 110
 Trp Asn Ser Gly Ser Ile Asp Thr Arg
 115 120

<210> 214
 <211> 193
 <212> PRT
 <213> Arabidopsis thaliana

<400> 214
 Met Thr Thr Thr Gly Ser Asn Ser Asn His Asn His His Glu Ser Asn
 1 5 10 15
 Asn Asn Asn Asn Asn Pro Ser Thr Arg Ser Trp Gly Thr Ala Val Ser
 20 25 30
 Gly Gln Ser Val Ser Thr Ser Gly Ser Met Gly Ser Pro Ser Ser Arg
 35 40 45
 Ser Glu Gln Thr Ile Thr Val Val Thr Ser Thr Ser Asp Thr Thr Phe
 50 55 60
 Gln Arg Leu Asn Asn Leu Asp Ile Gln Gly Asp Asp Ala Gly Ser Gln
 65 70 75 80
 Gly Ala Ser Gly Val Lys Lys Lys Lys Arg Gly Gln Arg Ala Ala Gly
 85 90 95
 Pro Asp Lys Thr Gly Arg Gly Leu Arg Gln Phe Ser Met Lys Val Cys
 100 105 110
 Glu Lys Val Glu Ser Lys Gly Arg Thr Thr Tyr Asn Glu Val Ala Asp
 115 120 125
 Glu Leu Val Ala Glu Phe Ala Leu Pro Asn Asn Asp Gly Thr Ser Pro
 130 135 140
 Asp Gln Gln Gln Tyr Asp Glu Lys Asn Ile Arg Arg Arg Val Tyr Asp
 145 150 155 160
 Ala Leu Asn Val Leu Met Ala Met Asp Ile Ile Ser Lys Asp Lys Lys
 165 170 175
 Glu Ile Gln Trp Arg Gly Leu Pro Arg Thr Ser Leu Ser Asp Ile Glu
 180 185 190

Glu

<210> 215
 <211> 81
 <212> PRT
 <213> Arabidopsis thaliana

<400> 215
 Gly Leu Pro Arg Thr Ser Leu Ser Asp Ile Glu Glu Leu Lys Asn Glu
 1 5 10 15
 Arg Leu Ser Leu Arg Asn Arg Ile Glu Lys Lys Thr Ala Tyr Ser Gln
 20 25 30
 Glu Leu Glu Glu Gln Tyr Val Gly Leu Gln Asn Leu Ile Gln Arg Asn
 35 40 45
 Glu His Leu Tyr Ser Ser Gly Asn Ala Pro Ser Gly Gly Val Ala Leu
 50 55 60
 Pro Phe Ile Leu Val Gln Thr Arg Pro His Ala Thr Val Glu Val Glu
 65 70 75 80
 Ile

<210> 216
 <211> 204
 <212> PRT
 <213> Arabidopsis thaliana

<400> 216
 Gly Leu Pro Arg Thr Ser Leu Ser Asp Ile Glu Glu Leu Lys Asn Glu
 1 5 10 15
 Arg Leu Ser Leu Arg Asn Arg Ile Glu Lys Lys Thr Ala Tyr Ser Gln
 20 25 30
 Glu Leu Glu Glu Gln Tyr Val Gly Leu Gln Asn Leu Ile Gln Arg Asn
 35 40 45
 Glu His Leu Tyr Ser Ser Gly Asn Ala Pro Ser Gly Gly Val Ala Leu
 50 55 60
 Pro Phe Ile Leu Val Gln Thr Arg Pro His Ala Thr Val Glu Val Glu
 65 70 75 80
 Ile Ser Glu Asp Met Gln Leu Val His Phe Asp Phe Asn Ser Thr Pro
 85 90 95
 Phe Glu Leu His Asp Asp Asn Phe Val Leu Lys Thr Met Lys Phe Cys
 100 105 110
 Asp Gln Pro Pro Gln Gln Pro Asn Gly Arg Asn Asn Ser Gln Leu Val
 115 120 125
 Cys His Asn Phe Thr Pro Glu Asn Pro Asn Lys Gly Pro Ser Thr Gly
 130 135 140
 Pro Thr Pro Gln Leu Asp Met Tyr Glu Thr His Leu Gln Ser Gln Gln
 145 150 155 160
 His Gln Gln His Ser Gln Leu Gln Ile Ile Pro Met Pro Glu Thr Asn
 165 170 175
 Asn Val Thr Ser Ser Ala Asp Thr Ala Pro Val Lys Ser Pro Ser Leu
 180 185 190
 Pro Gly Ile Met Asn Ser Ser Met Lys Pro Glu Asn
 195 200

<210> 217
 <211> 420
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 217
 Met Ser Gly Val Val Arg Ser Ser Pro Gly Ser Ser Gln Pro Pro Pro
 1 5 10 15
 Pro Pro Pro His His Pro Pro Ser Ser Pro Val Pro Val Thr Ser Thr
 20 25 30
 Pro Val Ile Pro Pro Ile Arg Arg His Leu Ala Phe Ala Ser Thr Lys
 35 40 45
 Pro Pro Phe His Pro Ser Asp Asp Tyr His Arg Phe Asn Pro Ser Ser
 50 55 60
 Leu Ser Asn Asn Asn Asp Arg Ser Phe Val His Gly Cys Gly Val Val
 65 70 75 80
 Asp Arg Glu Glu Asp Ala Val Val Val Arg Ser Pro Ser Arg Lys Arg
 85 90 95
 Lys Ala Thr Met Asp Met Val Val Ala Pro Ser Asn Asn Gly Phe Thr
 100 105 110
 Ser Ser Gly Phe Thr Asn Ile Pro Ser Ser Pro Cys Gln Thr Pro Arg
 115 120 125
 Lys Gly Gly Arg Val Asn Ile Lys Ser Lys Ala Lys Gly Asn Lys Ser
 130 135 140
 Thr Pro Gln Thr Pro Ile Ser Thr Asn Ala Gly Ser Pro Ile Thr Leu
 145 150 155 160
 Thr Pro Ser Gly Ser Cys Arg Tyr Asp Ser Ser Leu Gly Leu Leu Thr
 165 170 175
 Lys Lys Phe Val Asn Leu Ile Lys Gln Ala Lys Asp Gly Met Leu Asp
 180 185 190
 Leu Asn Lys Ala Ala Glu Thr Leu Glu Val Gln Lys Arg Arg Ile Tyr
 195 200 205
 Asp Ile Thr Asn Val Leu Glu Gly Ile Asp Leu Ile Glu Lys Pro Phe
 210 215 220
 Lys Asn Arg Ile Leu Trp Lys Gly Val Asp Ala Cys Pro Gly Asp Glu
 225 230 235 240
 Asp Ala Asp Val Ser Val Leu Gln Leu Gln Ala Glu Ile Glu Asn Leu
 245 250 255
 Ala Leu Glu Glu Gln Ala Leu Asp Asn Gln Ile Arg Gln Thr Glu Glu
 260 265 270
 Arg Leu Arg Asp Leu Ser Glu Asn Glu Lys Asn Gln Lys Trp Leu Phe
 275 280 285
 Val Thr Glu Glu Asp Ile Lys Ser Leu Pro Gly Phe Gln Asn Gln Thr
 290 295 300
 Leu Ile Ala Val Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp
 305 310 315 320
 Pro Asp Glu Ala Ala Asp His Pro Gln Arg Arg Tyr Arg Ile Ile Leu
 325 330 335
 Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Glu Phe Glu
 340 345 350
 Gly Lys Phe Glu Asp Thr Asn Gly Ser Gly Ala Ala Pro Pro Ala Cys
 355 360 365
 Leu Pro Ile Ala Ser Ser Ser Gly Ser Thr Gly His His Asp Ile Glu
 370 375 380
 Ala Leu Thr Val Asp Asn Pro Glu Thr Ala Ile Val Ser His Asp His
 385 390 395 400

Pro His Pro Gln Pro Gly Asp Thr Ser Asp Leu Asn Tyr Leu Gln Glu
 405 410 415
 Gln Val Gly Gly
 420

<210> 218
 <211> 324
 <212> PRT
 <213> Arabidopsis thaliana

<400> 218
 Pro Ser Gly Ser Cys Arg Tyr Asp Ser Ser Leu Gly Leu Leu Thr Lys
 1 5 10 15
 Lys Phe Val Asn Leu Ile Lys Gln Ala Lys Asp Gly Met Leu Asp Leu
 20 25 30
 Asn Lys Ala Ala Glu Thr Leu Glu Val Gln Lys Arg Arg Ile Tyr Asp
 35 40 45
 Ile Thr Asn Val Leu Glu Gly Ile Asp Leu Ile Glu Lys Pro Phe Lys
 50 55 60
 Asn Arg Ile Leu Trp Lys Gly Val Asp Ala Cys Pro Gly Asp Glu Asp
 65 70 75 80
 Ala Asp Val Ser Val Leu Gln Leu Gln Ala Glu Ile Glu Asn Leu Ala
 85 90 95
 Leu Glu Glu Gln Ala Leu Asp Asn Gln Ile Arg Gln Thr Glu Glu Arg
 100 105 110
 Leu Arg Asp Leu Ser Glu Asn Glu Lys Asn Gln Lys Trp Leu Phe Val
 115 120 125
 Thr Glu Glu Asp Ile Lys Ser Leu Pro Gly Phe Gln Asn Gln Thr Leu
 130 135 140
 Ile Ala Val Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp Pro
 145 150 155 160
 Asp Glu Ala Ala Asp His Pro Gln Arg Arg Tyr Arg Ile Ile Leu Arg
 165 170 175
 Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Glu Phe Glu Gly
 180 185 190
 Lys Phe Glu Asp Thr Asn Gly Ser Gly Ala Ala Pro Pro Ala Cys Leu
 195 200 205
 Pro Ile Ala Ser Ser Ser Gly Ser Thr Gly His His Asp Ile Glu Ala
 210 215 220
 Leu Thr Val Asp Asn Pro Glu Thr Ala Ile Val Ser His Asp His Pro
 225 230 235 240
 His Pro Gln Pro Gly Asp Thr Ser Asp Leu Asn Tyr Leu Gln Glu Gln
 245 250 255
 Val Gly Gly Met Leu Lys Ile Thr Pro Ser Asp Val Glu Asn Asp Glu
 260 265 270
 Ser Asp Tyr Trp Leu Leu Ser Asn Ala Glu Ile Ser Met Thr Asp Ile
 275 280 285
 Trp Lys Thr Asp Ser Gly Ile Asp Trp Asp Tyr Gly Ile Ala Asp Val
 290 295 300
 Ser Thr Pro Pro Pro Gly Met Gly Glu Ile Ala Pro Thr Ala Val Asp
 305 310 315 320
 Ser Thr Pro Arg

<210> 219

<211> 38
 <212> PRT
 <213> Arabidopsis thaliana

<400> 219
 Met Ser Gly Val Val Arg Ser Ser Pro Gly Ser Ser Gln Pro Pro Pro
 1 5 10 15
 Pro Pro Pro His His Pro Pro Ser Ser Pro Val Pro Val Thr Ser Thr
 20 25 30
 Pro Val Ile Pro Pro Ile
 35

<210> 220
 <211> 142
 <212> PRT
 <213> Arabidopsis thaliana

<400> 220
 Met Ser Met Glu Met Glu Leu Phe Val Thr Pro Glu Lys Gln Arg Gln
 1 5 10 15
 His Pro Ser Val Ser Val Glu Lys Thr Pro Val Arg Arg Lys Leu Ile
 20 25 30
 Val Asp Asp Asp Ser Glu Ile Gly Ser Glu Lys Lys Gly Gln Ser Arg
 35 40 45
 Thr Ser Gly Gly Gly Leu Arg Gln Phe Ser Val Met Val Cys Gln Lys
 50 55 60
 Leu Glu Ala Lys Lys Ile Thr Thr Tyr Lys Glu Val Ala Asp Glu Ile
 65 70 75 80
 Ile Ser Asp Phe Ala Thr Ile Lys Gln Asn Ala Glu Lys Pro Leu Asn
 85 90 95
 Glu Asn Glu Tyr Asn Glu Lys Asn Ile Arg Arg Arg Val Tyr Asp Ala
 100 105 110
 Leu Asn Val Phe Met Ala Leu Asp Ile Ile Ala Arg Asp Lys Lys Glu
 115 120 125
 Ile Arg Trp Lys Gly Leu Pro Ile Thr Cys Lys Lys Asp Val
 130 135 140

<210> 221
 <211> 150
 <212> PRT
 <213> Arabidopsis thaliana

<400> 221
 Glu Glu Val Lys Met Asp Arg Asn Lys Val Met Ser Ser Val Gln Lys
 1 5 10 15
 Lys Ala Ala Phe Leu Lys Glu Leu Arg Glu Lys Val Ser Ser Leu Glu
 20 25 30
 Ser Leu Met Ser Arg Asn Gln Glu Met Val Val Lys Thr Gln Gly Pro
 35 40 45
 Ala Glu Gly Phe Thr Leu Pro Phe Ile Leu Leu Glu Thr Asn Pro His
 50 55 60
 Ala Val Val Glu Ile Glu Ile Ser Glu Asp Met Gln Leu Val His Leu
 65 70 75 80
 Asp Phe Asn Ser Thr Pro Phe Ser Val His Asp Asp Ala Tyr Ile Leu
 85 90 95

Lys Leu Met Gln Glu Gln Lys Gln Glu Gln Asn Arg Val Ser Ser Ser
 100 105 110
 Ser Ser Thr His His Gln Ser Gln His Ser Ser Ala His Ser Ser Ser
 115 120 125
 Ser Ser Cys Ile Ala Ser Gly Thr Ser Gly Pro Val Cys Trp Asn Ser
 130 135 140
 Gly Ser Ile Asp Thr Arg
 145 150

<210> 222
 <211> 71
 <212> PRT
 <213> Arabidopsis thaliana

<400> 222
 Glu Glu Val Lys Met Asp Arg Asn Lys Val Met Ser Ser Val Gln Lys
 1 5 10 15
 Lys Ala Ala Phe Leu Lys Glu Leu Arg Glu Lys Val Ser Ser Leu Glu
 20 25 30
 Ser Leu Met Ser Arg Asn Gln Glu Met Val Val Lys Thr Gln Gly Pro
 35 40 45
 Ala Glu Gly Phe Thr Leu Pro Phe Ile Leu Leu Glu Thr Asn Pro His
 50 55 60
 Ala Val Val Glu Ile Glu Ile
 65 70

<210> 223
 <211> 262
 <212> PRT
 <213> Arabidopsis thaliana

<400> 223
 Met Thr Thr Thr Gly Ser Asn Ser Asn His Asn His His Glu Ser Asn
 1 5 10 15
 Asn Asn Asn Asn Asn Pro Ser Thr Arg Ser Trp Gly Thr Ala Val Ser
 20 25 30
 Gly Gln Ser Val Ser Thr Ser Gly Ser Met Gly Ser Pro Ser Ser Arg
 35 40 45
 Ser Glu Gln Thr Ile Thr Val Thr Ser Thr Ser Asp Thr Thr Phe
 50 55 60
 Gln Arg Leu Asn Asn Leu Asp Ile Gln Gly Asp Asp Ala Gly Ser Gln
 65 70 75 80
 Gly Ala Ser Gly Val Lys Lys Lys Lys Arg Gly Gln Arg Ala Ala Gly
 85 90 95
 Pro Asp Lys Thr Gly Arg Gly Leu Arg Gln Phe Ser Met Lys Val Cys
 100 105 110
 Glu Lys Val Glu Ser Lys Gly Arg Thr Thr Tyr Asn Glu Val Ala Asp
 115 120 125
 Glu Leu Val Ala Glu Phe Ala Leu Pro Asn Asn Asp Gly Thr Ser Pro
 130 135 140
 Asp Gln Gln Gln Tyr Asp Glu Lys Asn Ile Arg Arg Arg Val Tyr Asp
 145 150 155 160
 Ala Leu Asn Val Leu Met Ala Met Asp Ile Ile Ser Lys Asp Lys Lys
 165 170 175
 Glu Ile Gln Trp Arg Gly Leu Pro Arg Thr Ser Leu Ser Asp Ile Glu

[illegible]

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<210> 224
<211> 51
<212> PRT
<213> Arabidopsis thaliana
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<400> 224
Gly Val Asp Ala Cys Pro Gly Asp Glu Asp Ala Asp Val Ser Val Leu
1          5          10          15
Gln Leu Gln Ala Glu Ile Glu Asn Leu Ala Leu Glu Glu Gln Ala Leu
20          25          30
Asp Asn Gln Ile Arg Gln Thr Glu Glu Arg Leu Arg Asp Leu Ser Glu
35          40          45
Asn Glu Lys
50

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<210> 225
<211> 121
<212> PRT
<213> Arabidopsis thaliana
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<400>	225															
Gly	Val	Asp	Ala	Cys	Pro	Gly	Asp	Glu	Asp	Ala	Asp	Val	Ser	Val	Leu	
1				5					10					15		
Gln	Leu	Gln	Ala	Glu	Ile	Glu	Asn	Leu	Ala	Leu	Glu	Glu	Gln	Ala	Leu	
			20					25					30			
Asp	Asn	Gln	Ile	Arg	Gln	Thr	Glu	Glu	Arg	Leu	Arg	Asp	Leu	Ser	Glu	
		35					40					45				
Asn	Glu	Lys	Asn	Gln	Lys	Trp	Leu	Phe	Val	Thr	Glu	Glu	Asp	Ile	Lys	
	50					55					60					
Ser	Leu	Pro	Gly	Phe	Gln	Asn	Gln	Thr	Leu	Ile	Ala	Val	Lys	Ala	Pro	
65					70					75					80	
His	Gly	Thr	Thr	Leu	Glu	Val	Pro	Asp	Pro	Asp	Glu	Ala	Ala	Asp	His	
				85					90					95		
Pro	Gln	Arg	Arg	Tyr	Arg	Ile	Ile	Leu	Arg	Ser	Thr	Met	Gly	Pro	Ile	
			100					105					110			
Asp	Val	Tyr	Leu	Val	Ser	Glu	Phe	Glu								
		115					120									

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<210> 226
<211> 50
<212> PRT
<213> Arabidopsis thaliana
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<400> 226
 Gly Leu Asp Val Ser Lys Pro Gly Glu Thr Ile Glu Ser Ile Ala Asn
 1 5 10 15
 Leu Gln Asp Glu Val Gln Asn Leu Ala Glu Glu Ala Arg Leu Asp
 20 25 30
 Asp Gln Ile Arg Glu Ser Gln Glu Arg Leu Thr Ser Leu Ser Glu Asp
 35 40 45
 Glu Asn
 50

<210> 227
 <211> 118
 <212> PRT
 <213> Arabidopsis thaliana

<400> 227
 Gly Leu Asp Val Ser Lys Pro Gly Glu Thr Ile Glu Ser Ile Ala Asn
 1 5 10 15
 Leu Gln Asp Glu Val Gln Asn Leu Ala Ala Glu Glu Ala Arg Leu Asp
 20 25 30
 Asp Gln Ile Arg Glu Ser Gln Glu Arg Leu Thr Ser Leu Ser Glu Asp
 35 40 45
 Glu Asn Asn Lys Arg Leu Leu Phe Val Thr Glu Asn Asp Ile Lys Asn
 50 55 60
 Leu Pro Cys Phe Gln Asn Lys Thr Leu Ile Ala Val Lys Ala Pro His
 65 70 75 80
 Gly Thr Thr Leu Glu Val Pro Asp Pro Asp Glu Ala Gly Gly Tyr Gln
 85 90 95
 Arg Arg Tyr Arg Ile Ile Leu Arg Ser Thr Met Gly Pro Ile Asp Val
 100 105 110
 Tyr Leu Val Ser Gln Phe
 115

<210> 228
 <211> 393
 <212> DNA
 <213> Arabidopsis thaliana

<400> 228
 aatcgaatac tttggaaggg agttgatgcg tgtcctggcg atgaggatgc tgacgtatct 60
 gtattacagc tgcaggcaga aattgaaaac ctgcgcctcg aagagcaagc attagacaac 120
 caaatcagac aaacagagga aagattaaga gacctgagcg aaaatgaaaa gaatcagaaa 180
 tggctttttg taactgaaga ggatatcaag agtttaccag gtttcagaa ccagactctg 240
 atagccgtca aagotcctca tggcacaact ttggaagtgc ctgatccaga tgaagcggct 300
 gaccacccac aaaggagata caggatcatt cttagaagta caatgggacc tattgacgta 360
 tacctcgtca gcgaatttga agggaaattc gaa 393

<210> 229
 <211> 516
 <212> DNA
 <213> Arabidopsis thaliana

<400> 229

attattgcaa	gggataaaaa	ggaaatccgg	tggaaaggac	ttcctattac	ctgcaaaaag	60
gatgtggaag	aagtcaagat	ggatcgtaat	aaagttatga	gcagtgtgca	aaagaaggct	120
gcttttctta	aagagttgag	agaaaaggtc	tcaagtcttg	agagtcttat	gtcgagaaat	180
caagagatgg	ttgtgaagac	tcaaggccca	gcagaaggat	ttaccttacc	attcattcta	240
cttgagacaa	accctcacgc	agtagtcgaa	atcgagattt	ctgaagatat	gcaacttgta	300
cacctcgact	tcaatagcac	acctttctcg	gtccatgatg	atgcttacat	tttgaaactg	360
atgcaagaac	agaagcaaga	acagaacaga	gtatcttctt	cttcactctac	acatcaccaa	420
tctcaacata	gctccgctca	ttcttcatcc	agttcttgca	ttgcttctgg	aacctcaggc	480
ccggtttgct	ggaactcggg	atccattgat	actcgc			516

<210> 230
 <211> 276
 <212> DNA
 <213> Arabidopsis thaliana

<400> 230	
ggtcttcctc	ggacaagctt aagcgacatt gaagaattaa agaacgaacg actctcactt 60
aggaacagaa	ttgagaagaa aactgcatat tcccaagaac tggaagaaca agtaatgaac 120
atcatcgata	ctctcggtt atctgcttcc tgccttcaga atctgataca gagaaatgag 180
cacttatata	gctcaggaaa tgctcccagt ggcggtgttg ctcttccttt tctccttgct 240
cagactcgtc	ctcacgcaac agtagaagtg gagata 276

<210> 231
 <211> 645
 <212> DNA
 <213> Arabidopsis thaliana

<400> 231	
ggtcttcctc	ggacaagctt aagcgacatt gaagaattaa agaacgaacg actctcactt 60
aggaacagaa	ttgagaagaa aactgcatat tcccaagaac tggaagaaca agtaatgaac 120
atcatcgata	ctctcggtt atctgcttcc tgccttcaga atctgataca gagaaatgag 180
cacttatata	gctcaggaaa tgctcccagt ggcggtgttg ctcttccttt tctccttgct 240
cagactcgtc	ctcacgcaac agtagaagtg gagatatcag aagatatgca gctcgtgcat 300
tttgatttca	acagcactcc atttgagctc cagcagcaca attttgcct caagactatg 360
aagttttgtg	atcaaccgcc gcaacaacca aacggtcgga acaacagcca gctgggttgt 420
cacaatttca	cgccagaaaa ccctaacaaa ggccccagca cagggtccaac accgcagctg 480
gatatgtacg	agactcatct tcaatcgcaa caacatcagc agcattctca gctacaaatc 540
attcctatgc	ctgagactaa caacgttact tccagcgctg atactgctcc agtgaaatcc 600
ccgtctcttc	cagggataat gaactccagc atgaagccgg agaata 645

<210> 232
 <211> 450
 <212> DNA
 <213> Arabidopsis thaliana

<400> 232		
gaagaagtca	agatggatcg taataaagtt atgagcagtg tgcaaaagaa ggctgctttt 60	
cttaaagagt	tgagagaaaa ggtctcaagt cttgagagtc ttatgtcgag aaatcaagag 120	
atgggttgta	agactcaagg cccagcagaa ggatttacct taccattcat tctacttgag 180	
acaaaccctc	acgcagtagt cgaaatcgag atttctgaag atatgcaact tgtacacctc 240	
gacttcaata	gcacaccttt ctcggtccat gatgatgctt acattttgaa actgatgcaa 300	
gaacagaagc	aagaacagaa cagagtatct tcttcttcat ctacacatca ccaatctcaa 360	
catagctcgg	ctcattcttc atccagttct tgcattgctt ctggaacctc aggcccggtt 420	
tgctggaact	cgggatccat tgatactcgc	450

<210> 233
 <211> 213
 <212> DNA
 <213> Arabidopsis thaliana

<400> 233
 gaagaagtca agatggatcg taataaagtt atgagcagtg tgcaaaagaa ggctgctttt 60
 cttaaagagt tgagagaaaa ggtctcaagt cttgagagtc ttatgtcgag aaatcaagag 120
 atggttggtga agactcaagg cccagcagaa ggattttacct taccattcat tctacttgag 180
 acaaaccctc acgcagtagt cgaaatcgag att 213

<210> 234
 <211> 870
 <212> DNA
 <213> Arabidopsis thaliana

<400> 234
 atgacaacta ctgggtctaa ttctaatacac aaccaccatg aaagcaataa taacaacaat 60
 aaccctagta ctaggtcttg gggcacggcg gtttcaggtc aatctgtgtc tactagcggc 120
 agtatgggct ctccgtcgag ccggagtgag caaaccatca ccgttggtac atctactagc 180
 gacactactt ttcaacgcct gaataaattg gacattcaag gtgatgatgc tggttctcaa 240
 ggagcttctg gtgttaagaa gaagaagagg ggacagcgtg cggctgggtcc agataagact 300
 ggaagaggac tacgtcaatt tagtatgaaa ggtcttattc ctttctctgc ccctattatg 360
 ctttcattcta aatgcctttc aatttgtgaa aaggtggaaa gcaaagggaag gacaacttac 420
 aatgaggttg cagacgagct tgttgctgaa tttgcacttc caaataacga tggaaacatcc 480
 cctgatcagc aacagtatga tgagaaaaac ataagacgaa gagtatatga tgctttaaac 540
 gtcctcatgg ctatggatat aatatccaag gataaaaaag aaattcaatg gagaggtctt 600
 cctcggacaa gcttaagcga cattgaagaa tttaaagaacg aacgactctc acttaggaac 660
 agaattgaga agaaaactgc atattcccaa gaactggaag aacaagtaat gaacatcatc 720
 gatactctcg gcttatctgc ttcctgcctt cagaatctga tacagagaaa tgagcactta 780
 tatagctcag gaaatgctcc cagtggcggg gttgctcttc cttttatcct tgtccagact 840
 cgtcctcagc caacagtaga agtggagata 870

<210> 235
 <211> 153
 <212> DNA
 <213> Arabidopsis thaliana

<400> 235
 ggagttgatg cgtgtccttg cgatgaggat gctgacgtat ctgtattaca gctgcaggca 60
 gaaattgaaa acctcgccct cgaagagcaa gcattagaca accaaatcag acaaacagag 120
 gaaagattaa gagacctgag cgaaaatgaa aag 153

<210> 236
 <211> 363
 <212> DNA
 <213> Arabidopsis thaliana

<400> 236
 ggagttgatg cgtgtccttg cgatgaggat gctgacgtat ctgtattaca gctgcaggca 60
 gaaattgaaa acctcgccct cgaagagcaa gcattagaca accaaatcag acaaacagag 120
 gaaagattaa gagacctgag cgaaaatgaa aagaatcaga aatggctttt tgtaactgaa 180

gaggatatca agagtttacc aggtttccag aaccagactc tgatagccgt caaagctcct	240
catggcacaa ctttggaagt gcctgatcca gatgaagcgg ctgaccaccc acaaaggaga	300
tacaggatca ttcttagaag tacaatggga cctattgacg tatacctcgt cagcgaattt	360
gaa	363

<210> 237
 <211> 150
 <212> DNA
 <213> Arabidopsis thaliana

<400> 237	
ggtctcgatg tctcaaaaacc aggagaaaca atcgaaagca tagctaacct acaggatgaa	60
gtacaaaacc tcgcagctga ggaggcaaga ttagatgacc aaatcagaga atcacaagaa	120
agattaacaa gcttgagtga ggatgaaaac	150

<210> 238
 <211> 354
 <212> DNA
 <213> Arabidopsis thaliana

<400> 238	
ggtctcgatg tctcaaaaacc aggagaaaca atcgaaagca tagctaacct acaggatgaa	60
gtacaaaacc tcgcagctga ggaggcaaga ttagatgacc aaatcagaga atcacaagaa	120
agattaacaa gcttgagtga ggatgaaaac aaaaaaggt tactgttcgt cactgaaaac	180
gacattaaga acctaccatg cttccagaat aagacgctga tagctgtaaa ggcaccgcat	240
ggaacaactc ttgaggttcc agatcctgat gaggctgggtg gttatcagag gaggtacaga	300
atcattctga gaagcacaat gggaccaata gacgtgtacc tagtcagtca attc	354

<210> 239
 <211> 426
 <212> DNA
 <213> Arabidopsis thaliana

<400> 239	
atgagtatgg agatggagtt gtttgtcact ccagagaagc agaggcaaca tccttcagtg	60
agcgttgaga aaactccagt gagaaggaaa ttgattgttg atgatgattc tgaaattgga	120
tcagagaaga aagggcaatc aagaacttct ggaggcgggc ttcgtcaatt cagtgttatg	180
gtttgtcaga agttggaagc caagaagata actacttaca aggaggttgc agacgaaatt	240
atttcagatt ttgccacaat taagcaaaac gcagagaagc ctttgaatga aaatgagtac	300
aatgagaaga acataaggcg gagagtctac gatgcgctca atgtgttcat ggcgttggat	360
attattgcaa gggataaaaa ggaaatccgg tggaaaggac ttcctattac ctgcaaaaag	420
gatgtg	426

<210> 240
 <211> 7
 <212> PRT
 <213> artificial sequence

<220>
 <223> Description of Artificial Sequence: motif

<400> 240
 Met Lys Val Cys Glu Lys Val

1

5

<210> 241
<211> 8
<212> PRT
<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 241
Leu Asn Val Leu Met Ala Met Asp
1 5

<210> 242
<211> 8
<212> PRT
<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 242
Phe Asn Ser Thr Pro Phe Glu Leu
1 5

<210> 243
<211> 30
<212> DNA
<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 243
atagaattca tgaaagtttg tgaaaaggtg

30

<210> 244
<211> 33
<212> DNA
<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 244
atagaattcc tgaatgttct catggcaatg gat

33

<210> 245
<211> 33
<212> DNA
<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 245

ataggatccc agctcaaaag gagtgctatt gaa

33

<210> 246

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 246

ggggacaagt ttgtacaaaa aagcaggct

29

<210> 247

<211> 5

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 247

tcaca

5

<210> 248

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: motif

<400> 248

ggggaccact ttgtacaaga aagctgggt

29

<210> 249

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 249

atagaattca tgtccggtgt cgtacga

27

<210> 250

<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 250
ataggatccc acctccaatg tttctgcagc 30

<210> 251
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 251
atagaattcg agaagaaagg gcaatcaaga 30

<210> 252
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 252
atactgcaga gaaatctcga tttcgactac 30

<210> 253
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 253
gccactctca tagggttctc catcg 25

<210> 254
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 254
ggcatgcctc caagatcctt gaagt 25

<210> 255
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 255
gggtcttggt cgttttactg tt 22

<210> 256
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 256
ccaagacgat gacaacagat acagc 25

<210> 257
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 257
ataaaactaaa tcttcgctga a 21

<210> 258
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 258
caaacgcgga tctgaaaaac t 21

<210> 259
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 259
tctctcttcc aaatctcc 18

<210> 260
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 260
aagtctctca ctttctcact 20

<210> 261
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 261
ctaagctctc aagatcaaag gctta 25

<210> 262
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 262
ttaacattgc aaagagtttc aaggt 25

<210> 263
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: motif

<400> 263
Thr Pro Trp Lys
1

<210> 264
<211> 289
<212> PRT

<213> *Arabidopsis thaliana*

<400> 264

```

Met Gly Lys Tyr Ile Arg Lys Ser Lys Ile Asp Gly Ala Gly Ala Gly
1      5      10      15
Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ser Ser Ile Ala
20      25      30
Leu Met Asp Val Val Ser Pro Ser Ser Ser Ser Leu Gly Val Leu
35      40      45
Thr Arg Ala Lys Ser Leu Ala Leu Gln Gln Gln Gln Gln Arg Cys Leu
50      55      60
Leu Gln Lys Pro Ser Ser Pro Ser Ser Leu Pro Pro Thr Ser Ala Ser
65      70      75      80
Pro Asn Pro Pro Ser Lys Gln Lys Met Lys Lys Lys Gln Gln Gln Met
85      90      95
Asn Asp Cys Gly Ser Tyr Leu Gln Leu Arg Ser Arg Arg Leu Gln Lys
100     105     110
Lys Pro Pro Ile Val Val Ile Arg Ser Thr Lys Arg Arg Lys Gln Gln
115     120     125
Arg Arg Asn Glu Thr Cys Gly Arg Asn Pro Asn Pro Arg Ser Asn Leu
130     135     140
Asp Ser Ile Arg Gly Asp Gly Ser Arg Ser Asp Ser Val Ser Glu Ser
145     150     155     160
Val Val Phe Gly Lys Asp Lys Asp Leu Ile Ser Glu Ile Asn Lys Asp
165     170     175
Pro Thr Phe Gly Gln Asn Phe Phe Asp Leu Glu Glu Glu His Thr Gln
180     185     190
Ser Phe Asn Arg Thr Thr Arg Glu Ser Thr Pro Cys Ser Leu Ile Arg
195     200     205
Arg Pro Glu Ile Met Thr Thr Pro Gly Ser Ser Thr Lys Leu Asn Ile
210     215     220
Cys Val Ser Glu Ser Asn Gln Arg Glu Asp Ser Leu Ser Arg Ser His
225     230     235     240
Arg Arg Arg Pro Thr Thr Pro Glu Met Asp Glu Phe Phe Ser Gly Ala
245     250     255
Glu Glu Glu Gln Gln Lys Gln Phe Ile Glu Lys Tyr Asn Phe Asp Pro
260     265     270
Val Asn Glu Gln Pro Leu Pro Gly Arg Phe Glu Trp Thr Lys Val Asp
275     280     285
Asp

```

<210> 265

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 265

cgggccccaataatgattt

20

<210> 266

<211> 18

<212> DNA
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 266
gacacgggcc agagctgc

18

<210> 267
<211> 9
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 2,3,5 and 6
<223> Xaa = any amino acid

<220>
<221> VARIANT
<222> 7
<223> Xaa = Ile or Val

<220>
<221> VARIANT
<222> 8
<223> Xaa = any amino acid or a stretch of any two
subsequent amino acids

<220>
<223> Description of Artificial Sequence: motif

<400> 267
Arg Xaa Xaa Leu Xaa Xaa Xaa Xaa Asn
1 5

<210> 268
<211> 8
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 3
<223> Xaa = any amino acid

<220>
<221> VARIANT
<222> 6
<223> Xaa = Ile or Val

<220>
<223> Description of Artificial Sequence: motif

<400> 268

Met Arg Xaa Ile Leu Xaa Asp Trp
1 5

<210> 269

<211> 8

<212> PRT

<213> artificial sequence

<220>

<221> VARIANT

<222> 5,6,7

<223> Xaa = any amino acid

<220>

<223> Description of Artificial Sequence: motif

<400> 269

Lys Tyr Glu Glu Xaa Xaa Xaa Pro
1 5

<210> 270

<211> 9

<212> PRT

<213> artificial sequence

<220>

<221> VARIANT

<222> 2,4,5,7

<223> Xaa = any amino acid

<220>

<223> Description of Artificial Sequence: motif

<400> 270

Gly Xaa Gly Xaa Xaa Gly Xaa Val Tyr
1 5

<210> 271

<211> 10

<212> PRT

<213> artificial sequence

<220>

<221> VARIANT

<222> 4,6,7,9

<223> Xaa = any amino acid

<220>

<223> Description of Artificial Sequence: motif

<400> 271

His Arg Asp Xaa Lys Xaa Xaa Asn Xaa Leu
1 5 10

<210> 272
<211> 11
<212> PRT

<213> artificial sequence

<220>
<221> VARIANT
<222> 2
<223> Xaa = any amino acid or a stretch of any two
subsequent amino acids

<220>
<221> VARIANT
<222> 5,7,8,9,10
<223> Xaa = any amino acid

<220>
<221> VARIANT
<222> 3
<223> Xaa = Trp or Tyr

<220>
<223> Description of Artificial Sequence: motif

<400> 272
Asp Xaa Xaa Ser Xaa Gly Xaa Xaa Xaa Xaa Glu
1 5 10

<210> 273
<211> 4
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 3
<223> Xaa = amino acid or a stretch of any two
subsequent amino acids

<220>
<221> VARIANT
<222> 4
<223> Xaa = Arg or Lys

<220>
<223> Description of Artificial Sequence: motif

<400> 273
Thr Pro Xaa Xaa
1

<210> 274

<211> 4
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 3
<223> Xaa = any amino acid

<220>
<221> VARIANT
<222> 4
<223> Xaa = Arg or Lys

<220>
<223> Description of Artificial Sequence: motif

<400> 274
Ser Pro Xaa Xaa
1

<210> 275
<211> 4
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 3
<223> Xaa = any amino acid

<220>
<221> VARIANT
<222> 4
<223> Xaa = Ile, Leu, Val or Met

<220>
<223> Description of Artificial Sequence: motif

<400> 275
Ser Pro Xaa Xaa
1

<210> 276
<211> 4
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 3
<223> Xaa = Ile, Leu, Val or Met

<220>
<221> VARIANT

<222> 4
<223> Xaa = any amino acid

<220>
<223> Description of Artificial Sequence: motif

<400> 276
Ser Pro Xaa Xaa
1

<210> 277
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: motif

<400> 277
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 278
<211> 7
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 3
<223> Xaa may be a stretch of any ten subsequent amino
acids

<220>
<223> Description of Artificial Sequence: motif

<400> 278
Lys Arg Xaa Lys Lys Lys Lys
1 5

<210> 279
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: motif

<400> 279
Lys Arg Pro Arg Pro
1 5

<210> 280

<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> Description of Artificial Sequence: motif

<400> 280
Pro Ala Ala Lys Arg Val Lys Leu Asp
1 5

<210> 281
<211> 4
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 2,3
<223> Xaa = any amino acid

<220>
<223> Description of Artificial Sequence: motif

<400> 281
Arg Xaa Xaa Phe
1

<210> 282
<211> 5
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 2,4
<223> Xaa = any amino acid

<220>
<223> Description of Artificial Sequence: motif

<400> 282
Leu Xaa Cys Xaa Glu
1 5

<210> 283
<211> 5
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 2,4
<223> Xaa = any amino acid

<220>

<223> Description of Artificial Sequence: motif

<400> 283

Leu Xaa Ser Xaa Glu

1

5

<210> 284

<211> 9

<212> PRT

<213> artificial sequence

<220>

<221> VARIANT

<222> 3

<223> Xaa may be a stretch of any seven subsequent amino acids

<220>

<221> VARIANT

<222> 5

<223> Xaa may be a stretch of any three subsequent amino acids

<220>

<223> Description of Artificial Sequence: motif

<400> 284

Asp Tyr Xaa Glu Xaa Asp Leu Phe Asp

1

5

<210> 285

<211> 9

<212> PRT

<213> artificial sequence

<220>

<221> VARIANT

<222> 3

<223> Xaa may be a stretch of any six subsequent amino acids

<220>

<221> VARIANT

<222> 5

<223> Xaa may be a stretch of any four subsequent amino acids

<220>

<223> Description of Artificial Sequence: motif

<400> 285

Asp Tyr Xaa Asp Xaa Asp Met Trp Glu

1

5

<210> 286
<211> 35
<212> PRT
<213> artificial sequence

<220>
<221> VARIANT
<222> 1
<223> Xaa may be Asp, Asn or no amino acid

<220>
<221> VARIANT
<222> 2
<223> Xaa = Gln or Glu

<220>
<221> VARIANT
<222> 7
<223> Xaa = Arg or Gly

<220>
<221> VARIANT
<222> 10
<223> Xaa = be Tyr or Asp

<220>
<221> VARIANT
<222> 16
<223> Xaa = Leu or Phe

<220>
<221> VARIANT
<222> 19
<223> Xaa = Met, Ile, Leu or no amino acid

<220>
<221> VARIANT
<222> 20
<223> Xaa = Asp or Asn

<220>
<221> VARIANT
<222> 21
<223> Xaa = Val or Ile

<220>
<221> VARIANT
<222> 23
<223> Xaa = be Ser or Ala

<220>
<221> VARIANT
<222> 24
<223> Xaa = Lys or Arg

<220>

<221> VARIANT

<222> 25

<223> Xaa = Asp or Glu

<220>

<221> VARIANT

<222> 30

<223> Xaa = Lys, Gln, Arg or no amino acid

<220>

<221> VARIANT

<222> 32

<223> Xaa = Arg, Lys or Ile

<220>

<223> Description of Artificial Sequence: motif

<400> 286

Xaa Xaa Lys Asn Ile Arg Xaa Arg Val Xaa Asp Ala Leu Asn Val Xaa
1 5 10 15
Met Ala Xaa Xaa Xaa Ile Xaa Xaa Xaa Lys Lys Glu Ile Xaa Trp Xaa
20 25 30
Gly Leu Pro
35

<210> 287

<211> 37

<212> PRT

<213> artificial sequence

<220>

<221> VARIANT

<222> 1

<223> Xaa = Gly or Asn

<220>

<221> VARIANT

<222> 2

<223> Xaa = Lys or Arg

<220>

<221> VARIANT

<222> 6

<223> Xaa = His or Gln

<220>

<221> VARIANT

<222> 9

<223> Xaa = Met or Val

<220>

<221> VARIANT

<222> 10

<223> Xaa = Lys or Met

<220>
<221> VARIANT
<222> 11
<223> Xaa = Ile or Val

<220>
<221> VARIANT
<222> 12
<223> Xaa may be a stretch of any zero to seventeen
subsequent amino acid

<220>
<221> VARIANT
<222> 14
<223> Xaa = Glu or Gln

<220>
<221> VARIANT
<222> 16
<223> Xaa = Val or Leu

<220>
<221> VARIANT
<222> 17
<223> Xaa = Gln, Glu or no amino acid

<220>
<221> VARIANT
<222> 18
<223> Xaa = Ser or no amino acid

<220>
<221> VARIANT
<222> 19
<223> Xaa = any amino acid

<220>
<221> VARIANT
<222> 21
<223> Xaa = Gly or Lys

<220>
<221> VARIANT
<222> 22
<223> Xaa = Arg, Ile or no amino acid

<220>
<221> VARIANT
<222> 25
<223> Xaa = Ser or no amino acid

<220>
<221> VARIANT
<222> 27
<223> Xaa = Asn or Lys

<220>

<221> VARIANT
 <222> 33
 <223> Xaa = Leu or Ile

<220>
 <221> VARIANT
 <222> 34
 <223> Xaa = Val or Ile

<220>
 <221> VARIANT
 <222> 35
 <223> Xaa = Ala or Ser

<220>
 <221> VARIANT
 <222> 36
 <223> Xaa = Glu or Gln

<220>
 <223> Description of Artificial Sequence: motif

<400> 287
 Xaa Xaa Gly Leu Arg Xaa Phe Ser Xaa Xaa Xaa Xaa Cys Xaa Lys Xaa
 1 5 10 15
 Xaa Xaa Xaa Lys Xaa Xaa Thr Thr Xaa Tyr Xaa Glu Val Ala Asp Glu
 20 25 30
 Xaa Xaa Xaa Xaa Phe
 35

<210> 288
 <211> 9
 <212> PRT
 <213> artificial sequence

<220>
 <221> VARIANT
 <222> 1
 <223> Xaa = Arg or Ser

<220>
 <221> VARIANT
 <222> 2
 <223> Xaa = Ile or Val

<220>
 <221> VARIANT
 <222> 3, 6, 8
 <223> Xaa = any amino acid

<220>
 <221> VARIANT
 <222> 4
 <223> Xaa = Gln or Lys

<220>

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<221>  VARIANT
<222>  7
<223>  Xaa = Leu or Ser
```

<220>
<223> Description of Artificial Sequence: motif

<400> 288
Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Glu
1 5

```
<210> 289
<211> 19
<212> PRT
<213> artificial sequence
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```
<220>
<221> VARIANT
<222> 1
<223> Xaa = Arg or Ser
```

```
<220>
<221> VARIANT
<222> 2
<223> Xaa = Ile or Val
```

```
<220>
<221>  VARIANT
<222>  3,5,8
<223>  Xaa = any amino acid
```

```
<220>
<221> VARIANT
<222> 4
<223> Xaa = Gln or Lys
```

```
<220>
<221>  VARIANT
<222>  6
<223>  Xaa may be a stretch of any three subsequent amino
      acids
```

```
<220>
<221> VARIANT
<222> 7
<223> Xaa = Leu or Ser
```

```
<220>
<221> VARIANT
<222> 10
<223> Xaa = Leu or Met
```

```
<220>
<221> VARIANT
<222> 11
<223> Xaa may be a stretch of any of two or three
```

subsequent amino acids

<220>

<221> VARIANT

<222> 12

<223> Xaa = Gln or His

<220>

<221> VARIANT

<222> 13

<223> Xaa may be a stretch of any of four or five
subsequent amino acids

<220>

<221> VARIANT

<222> 16

<223> Xaa = Val, Ile or Met

<220>

<221> VARIANT

<222> 17

<223> Xaa = Gln or Glu

<220>

<223> Description of Artificial Sequence: motif

<400> 289

Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Asn Leu Xaa

1

5

10

15

Xaa Arg Asn

<210> 290

<211> 26

<212> PRT

<213> artificial sequence

<220>

<221> VARIANT

<222> 1,5

<223> Xaa = Leu or Ile

<220>

<221> VARIANT

<222> 6

<223> Xaa = Val or Leu

<220>

<221> VARIANT

<222> 7,25

<223> Xaa = amino acid

<220>

<221> VARIANT

<222> 9

<223> Xaa may be a stretch of any of three or four

subsequent amino acids

<220>

<221> VARIANT

<222> 10

<223> Xaa = Thr or Val

<220>

<221> VARIANT

<222> 12

<223> Xaa may be a stretch of any of twelve to fourteen subsequent amino acids

<220>

<221> VARIANT

<222> 14

<223> Xaa may be a stretch of any of three or four subsequent amino acids

<220>

<221> VARIANT

<222> 16

<223> Xaa = Glu or Ser

<220>

<221> VARIANT

<222> 17

<223> Xaa = Met, Ile, Val or Leu

<220>

<221> VARIANT

<222> 21

<223> Xaa may be a stretch of any of two subsequent amino acids

<220>

<221> VARIANT

<222> 22

<223> Xaa = Val or Ile

<220>

<221> VARIANT

<222> 24

<223> Xaa = Arg or Lys

<220>

<223> Description of Artificial Sequence: motif

<400> 290

Xaa	Pro	Phe	Ile	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Val	Xaa	Phe	Xaa	Phe	Xaa
1				5					10					15	
Xaa	His	Asp	Asp	Xaa	Xaa	Leu	Xaa	Xaa	Met						
				20					25						

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International Bureau



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- (74) Agent: DE CLERCQ, Ann; De Clercq, Brants & Partners, E. Gevaertdreef 10 a, B-9830 Sint-Martens-Latem (BE).
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- Published:
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(54) Title: NUCLEIC ACID MOLECULES ENCODING PLANT CELL CYCLE PROTEINS AND USES THEREFOR

(57) Abstract: The invention provides isolated nucleic acids molecules, designated CCP nucleic acid molecules, which encode novel cell cycle associated polypeptides. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing CCP nucleic acid molecules, host cells into which the expression vectors have been introduced, and transgenic plants in which a CCP gene has been introduced or disrupted. The invention still further provides isolated CCP proteins, fusion proteins, antigenic peptides and anti-CCP antibodies. Agricultural, diagnostic, screening, and therapeutic methods utilizing compositions of the invention are also provided.

WO 01/085946 A3

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01307

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/29 C12N15/82 C07K14/415 C07K16/16 G01N33/68
C12Q1/68 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K G01N C12Q A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, PAJ, WPI Data, SEQUENCE SEARCH, BIOSIS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL [Online] EBI, Hinxton, UK; 2 November 1994 (1994-11-02) SZARKA S J ET AL: "Characterization of a cyclin domain containing gene family in Brassica napus" Database accession no. L25405 XP002211934 abstract	3-12,14, 21
X	--- DATABASE EMBL [Online] EBI Hinxton, UK; 18 December 1994 (1994-12-18) LU G AND FERL R J: "An Arabidopsis cDNA clone encoding cyclin" Database accession no. U17890 XP002211935 abstract --- -/-	3-12,14, 21

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

2 September 2002

Date of mailing of the international search report

20 11 2002

Name and mailing address of the ISA

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01307

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL [Online] EBI Hinxton, UK; 10 June 1995 (1995-06-10) KOUCHI H ET AL: "Distinct classes of mitotic cyclins are differentially expressed in the soybean shoot apex during the cell cycle" Database accession no. D50869 XP002211936 abstract -& KOUCHI H ET AL.: PLANT CELL, vol. 7, 1995, pages 1143-1155, XP002211933 the whole document</p>	3-12, 19-21
X	<p>--- DATABASE EMBL [Online] EBI, Hinxton, UK; 13 November 1999 (1999-11-13) FEDERSPIEL N A ET AL: "Arabidopsis thaliana chromosome I BAC T16N11 genomic sequence" Database accession no. AC013453 XP002211937 abstract</p>	3-12, 14, 21
A	<p>--- WO 99 64599 A (FOWKE LARRY C ;WANG HONG (CA); CANADA AGRICULTURE (CA); CANADA NAT) 16 December 1999 (1999-12-16) the whole document</p>	1-45
A	<p>--- WO 99 14331 A (ALMEIDA JANICE DE ;LANDRIEU ISABELLE (BE); VEYLDER LIEVEN DE (BE);) 25 March 1999 (1999-03-25) the whole document</p>	1-45
A	<p>--- WO 99 13083 A (VEYLDER LIEVEN DE ;INZE DIRK (BE); CROPDESIGN N V (BE); SEGERS GER) 18 March 1999 (1999-03-18) the whole document</p>	1-45
A	<p>--- WO 92 09685 A (UNIV AUSTRALIAN) 11 June 1992 (1992-06-11) the whole document</p>	1-45
A	<p>--- WO 99 22002 A (ALMEIDE JANICE DE ;VEYLDER LIEVEN DE (BE); INZE DIRK (BE); CROPDES) 6 May 1999 (1999-05-06) the whole document</p> <p>---</p>	1-45

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01307

C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>MIRONOV V ET AL: "Cyclin-dependent kinases and cell division in plants-the nexus"</p> <p>PLANT CELL, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, US, vol. 11, April 1999 (1999-04), pages 509-521, XP002126400</p> <p>ISSN: 1040-4651</p> <p>the whole document</p> <p style="text-align: center;">-----</p>	1-45

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 01/01307

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 18, 24, 30-32, 35, 39-45
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-45 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-45 partially

A nucleic acid comprising SEQ ID NO: 3 or 41 and a polypeptide encoded by said nucleic acid comprising SEQ ID NO: 69 (CCP3). A vector, a cell, a host cell, a method of producing a polypeptide, an antibody, a method of detecting the presence, a kit, a method for identifying a compound, a method for modulating the activity, a transgenic plant, a method for modulating the growth of a plant, a method for modulating the cell cycle in a plant comprising said nucleic acid or polypeptide.

2. Claims: 1-45 partially

same as invention 1 but comprising SEQ ID NO: 6, 42, 72 and 108 (CCP6).

3. Claims: 1-45 partially

same as invention 1 but comprising SEQ ID NO: 12, 13, 45, 78, 79 and 111 (CCP12/13).

4. Claims: 1-45 partially

same as invention 1 but comprising SEQ ID NO: 29 and 95 (CCP29).

5. Claims: 30-45 partially

A method for modulating the growth of a plant, a method for modulating the cell cycle in a plant comprising a CCP modulator with SEQ 1, 39, 67 and 105 (CCP1).

6. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 2, 40, 68 and 106 (CCP2).

7. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 4 and 70 (CCP4).

8. Claims: 30-45 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 5 but comprising SEQ ID NO: 5 and 71
(CCP5).

9. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 7, 8, 42, 43,
72, 73, 108 and 109 (CCP7/8).

10. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 9 and 75
(CCP9).

11. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 10 and 76
(CCP10).

12. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 11, 44, 77 and
110 (CCP11).

13. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 14, 46, 80 and
112 (CCP14).

14. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 15, 47, 81 and
113 (CCP15).

15. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 16, 48, 82 and
114 (CCP16).

16. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 17 and 83
(CCP17).

17. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 18, 49, 84 and

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

115 (CCP18).

18. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 19 and 85 (CCP19).

19. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 20, 21, 50, 86, 87 and 116 (CCP20/21).

20. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 22, 51, 88 and 117 (CCP22).

21. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 23, 52, 89 and 118 (CCP23).

22. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 24, 53, 90 and 119 (CCP24).

23. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 25, 54, 91 and 120 (CCP25).

24. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 26, 55, 92 and 121 (CCP26).

25. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 27, 56, 93 and 122 (CCP27).

26. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 28, 57, 94 and 123 (CCP28).

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

27. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 30, 58, 96 and 124 (CCP30).

28. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 31, 59, 97 and 125 (CCP31).

29. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 32, 60, 98 and 125 (CCP32).

30. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 33, 61, 99 and 127 (CCP33).

31. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 34, 62, 100 and 128 (CCP34).

32. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 35, 63, 101 and 129 (CCP35).

33. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 36, 64, 102 and 130 (CCP36).

34. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 37, 65, 103 and 131 (CCP37).

35. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 38, 66, 104 and 132 (CCP38).

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

36. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 205, 224, 225, 228, 235 and 236 (AtE2Fa).

37. Claims: 30-45 partially

same as invention 5 but comprising SEQ ID NO: 211, 220-222, 229, 232, 233 and 239 (AtDPa).

38. Claims: 30-45 partially

same as invention 1 but comprising SEQ ID NO: 215, 216, 223, 230, 231 and 234 (AtDPb).

39. Claims: 30-45 partially

same as invention 1 but comprising SEQ ID NO: 226, 227, 237 and 238 (AtE2Fb).

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 18, 24, 30-32, 35, 39-45

Present claims 18, 24, 30-32, 35, 39-45 relate to a product/compound defined by reference to a desirable characteristic or property, namely a compound that binds to a polypeptide or a CCP modulator. The claims cover all products/compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such products/compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the product/compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to the products/ compounds antibodies, mutated variants of the polypeptide, antisense nucleic acid and ribozyme mentioned in the description at pages 38-43, 47-52.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 01/01307

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9964599	A	16-12-1999	AU 4126999 A CA 2329684 A1 WO 9964599 A1 EP 1086226 A1 US 2001025379 A1	30-12-1999 16-12-1999 16-12-1999 28-03-2001 27-09-2001
WO 9914331	A	25-03-1999	AU 9540698 A CA 2303759 A1 WO 9914331 A2 EP 1015590 A2 JP 2001516582 T	05-04-1999 25-03-1999 25-03-1999 05-07-2000 02-10-2001
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